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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 02:52:41 ; Search time 9525 Seconds
(without alignments)
11079.838 Million cell updates/sec

Title: US-10-617-623-1
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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: gb_sta.*
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14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 16 | 832.8 | 38.2 | 2637 | 8 | AB038492 | AB038492 Atriplex |
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| 23 | 806.4 | 37.0 | 2263 | 8 | AF370358 | AF370358 Suaeda ma |
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ALIGNMENTS

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DEFINITION Sequence 2125 from Patent WO2004035798.
ACCESSION CQ805714
VERSION CQ805714.1 GI:47111491
KEYWORDS Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1
AUTHORS Inze,D., de Veylder,L. and Vlieghe,K.
TITLE Identification of novel e2f target genes and use thereof
JOURNAL Patent: WO 2004035798-A 2125 29-APR-2004;
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Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ACCESSION AX506544
 VERSION AX506544.1 GI:23387781
 KEYWORDS Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1
 AUTHORS Harper, J. F., Kreps, J., Wang, X. and Zhu, T.
 TITLE Stress-regulated genes of plants, transgenic plants containing same, and methods of use
 JOURNAL Patent: WO 0216655-A 1239 28-FEB-2002;
 The Scripps Research Institute (US); Syngenta Participations AG (CH)
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 Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 3
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DEFINITION Arabidopsis thaliana Na+/H+ exchanger (NHX1) mRNA, complete cds.
ACCESSION AF056190
VERSION AF056190.1 GI:6650176
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 1619)
AUTHORS Quintero, F.J., Blatt, M.R. and Pardo, J.M.
TITLE Functional conservation between yeast and plant endosomal Na(+)/H(+) antiporters
JOURNAL FEBS Lett. 471 (2-3), 224-228 (2000)
MEDLINE 20231718
PUBMED 10767428
REFERENCE 2 (bases 1 to 1619)
AUTHORS Quintero, F.J.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-1998) Biologia Vegetal, IRNASE (CSIC), Avda.
Reina Mercedes s/n, Sevilla 41012, Spain

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ORIGIN
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Best Local Similarity 99.9%; Pred. No. 0;
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RESULT 4
AF106324

LOCUS AF106324 1614 bp mRNA linear PLN 03-MAR-1999
DEFINITION Arabidopsis thaliana sodium proton exchanger Nhx1 mRNA, partial cds.
ACCESSION AF106324
VERSION AF106324.1 GI:4324596
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1614)
Gaxiola, R.A., Rao, R., Sherman, A., Grisafi, P., Alper, S.L. and Fink, G.R.

REFERENCE 1 The Arabidopsis thaliana proton transporters, AtNhx1 and Avp1, can function in cation detoxification in yeast
Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1480-1485 (1999)
99145575
PUBMED 9990049

2 (bases 1 to 1614)

Gaxiola, R.A., Rao, R., Sherman, A., Grisafi, P., Alper, S.L. and Fink, G.R.

Direct Submission

Submitted (12-NOV-1998) Whitehead, Nine Cambridge Center,

Cambridge, MA 02142, USA

Location/Qualifiers

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Matches 1614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 346 | GTTCGCTTGAATCTCTTTGTTGCACTCTTTTGTCTGTTATGTTCTTGTGTCATCTTTT | 405 |
| Db | 61 | GTTCGCTTGAATCTCTTTGTTGCACTCTTTTGTCTGTTATGTTCTTGTGTCATCTTTT | 120 |
| Qy | 406 | GAAGAGATAGATGATGAACGAATCCATCACCGCTTTGTTGATTTGGCTAGGCATCTGT | 465 |
| Db | 121 | GAAGAGATAGATGATGAACGAATCCATCACCGCTTTGTTGATTTGGCTAGGCATCTGT | 180 |
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| Db | 541 | GGTGTGTGATGATCAACGTCAGTGTGCTTTCAACCGGATTCAGACCTTTGATCTC | 600 |
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| Db | 661 | CTAAGTACCTTGTGTTGCTGCAACCGGTCGATAGTGCCTATGTTATCAAGAGCTA | 720 |
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| Db | 1201 | AAGTTTACAGGGCCGGGCAACAGATGTACGGGGAATGCAATCATGATCAGAGTACG | 1260 |
| Qy | 1546 | ATAACTGTCTCTTTTATAGCAGTGGTGTGTTGGTATGCTGACCAACCACTCATTAAC | 1605 |
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| Db | 1381 | TCATACATATATCTTTTGTGGACCAAGACTCGTTTATGAGGCTTTCAGGGAACCAAT | 1440 |
| Qy | 1726 | GTGCTCGGCTGACAGTATACGTGGCTTCTTACACGGCCCACTGGAACCGTGCAATAC | 1785 |
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| Db | 1561 | CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCTGATCTTAGTAAGGCT | 1614 |

RESULT 5

AY685183

LOCUS

DEFINITION

Arabidopsis thaliana

cds.

AY685183

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana

Arabidopsis thaliana

Eukaryota; Viridiplantae;

Spermatophyta; Magnoliophyta;

rosids; eurosids II; Brassicales;

Brassicaceae; Arabidopsi

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

gene

AY685183 1617 bp mRNA linear PLN 16-AUG-2004
Arabidopsis thaliana sodium proton exchanger (NHX1) mRNA, complete cds.

AY685183

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana

Arabidopsis thaliana

Eukaryota; Viridiplantae;

Spermatophyta; Magnoliophyta;

rosids; eurosids II; Brassicales;

Brassicaceae; Arabidopsi

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AUTHORS

TITLE

JOURNAL

FEATURES

Source

gene

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AUTHORS Baek,S.H.
TITLE Isolation and characterization of a Na⁺/H⁺ antiporter gene from Arabidopsis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1617)
AUTHORS Baek,S.H., Kim,H.S., Lee,Y.T., Lee,M.H. and Yun,S.J.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Rice Research Division, National Honam Agricultural Experiment Station, Songhak-dong, Iksan, Jeonbuk 570-080, Republic of Korea

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DB 61 GTTGCCTTGAATCTCTTTGTGCACTTCTTTGTGCTTGTATTGTTCTTGGTCACTTTTG 120
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DB 121 GAAGAGATAGATGGAACGAATCCATCACCCTTGTGATTGGGCTAGGCACCTAGT 180
QY 466 GTTACCAATTTGTGATTAGTAAGGAAGAAAGCTCCGATCTCTCGTCTTTAGTGAAGAT 525
DB 181 GTTACCAATTTGTGATTAGTAAGGAAGAAAGCTCCGATCTCTCGTCTTTAGTGAAGAT 240
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RESULT 8
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LOCUS      Arabidopsis thaliana Na+/H+ exchanger 2 (NHX2) mRNA, complete cds.
ACCESSION      AF490586
VERSION      AF490586.1 GI:19919839
KEYWORDS
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1641)
REFERENCE      Yokoi,S., Quintero,F.J., Cubero,B., Ruiz,T., Bressan,R.A.,
AUTHORS      Hasegawa,P.M. and Pardo,J.M.
TITLE      Differential expression and function of Arabidopsis thaliana NHX
Na+/H+ antiporters in the salt stress response
JOURNAL      Plant J. (2002) In press
REFERENCE      2 (bases 1 to 1641)
AUTHORS      Quintero,F.J., Cubero,B. and Pardo,J.M.
TITLE      Direct Submission
JOURNAL      Submitted [07-MAR-2002] Biologia Vegetal, IRNASE-CSIC, Avda. Reina
Mercedes, 10, Sevilla, Sevilla 41012, Spain
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ORIGIN

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Qy      400 CTTTTCGAAGAGAATAGATGGAATGAACGAATCCATCACCGCCTTGTGTATGGGCTAGGC 459
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Qy      880 GATCTCACTCACTAAACCAACGAGCTGCTTTTCACTCTCTTGAAACTCTTGTGATTTC 939
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Qy      1060 TATCTTTCTATATGCTGCTGAGCTTTTCGACTTCGAGCGGTATCCTCACTGTGTTTTC 1119
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Qy      1300 ATCGCAGTGAGCTCAATCCTTAATGGGTCTGGTCAATGTTGGAGAGACAGGCTTCGCTTTT 1359
Db      1021 GTTGCAGTGAGCTCAATCCTTAATGGGTCTAGTCACTGCTTGGAGAGACAGCTTTTGTCTTT 1080
Qy      1360 CCGTTATCGTTCTTATCTTAACCTTAGCCAAAGAGAAATCAAGCGGAGAAATCACTTTAAC 1419
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| Qy | 1480 | TACAACAAGTTTACAAAGGCCGGGACACAGATGTAACGCGGGAATCAATCATGATCAAG | 1539 |
| Db | 1201 | TACAATAAAGTTTACAAGAATCAGGGCACACAGAAATGCGCGGAATGCAATCATGATTACC | 1260 |
| Qy | 1540 | AGTACGATAACTGTCTGCTTTTTAGACACAGTGTGTTTGATATGCTGACCAACCACTC | 1599 |
| Db | 1261 | AGTACAATACCGTCTGCTTTTTAGACCAATGCTGTTTGATATGCTTAAACAACCACTG | 1320 |
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| Db | 1321 | ATTAGATACTTAATGCCACACCAAAAAGCACCACAGTACCAGAGTATGTTATCGGAC | 1380 |
| Qy | 1651 | GACAACACCCCAAAATCCATACATATCCCTTTGTTGG-----ACCAAGACTCGTTC | 1701 |
| Db | 1381 | GATAGCACTCGGAAATCAATCCATATCCGCTCTCTGATGGTAGACAGCTAGATTCAATTT | 1440 |
| Qy | 1702 | ATTGAGCGCTTCAGGGAACCAATATGTCCTCGGCCTGACAGTATACGTGTCTTTTGACA | 1761 |
| Db | 1441 | GAGTTACTTGGAGCCACCAGGAGCTGCCACGACCAACAGCCTTCGAGTTTCTCTCATG | 1500 |
| Qy | 1762 | CGGCCCACTCGAACCGTGCAATTACTGTGAGACAATTTGATGACTCTTTCATGCGAACCC | 1821 |
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| Qy | 1822 | GTCTTTGGAGGTCTGTGGCTTTGTACCCCTTTGTTCCAGGTTTCTCCAATGAGAGAAACCTT | 1881 |
| Db | 1561 | GTGTTTGGTGGTCCGGAATTCGTTCCTCTTGTCCCTGGTTCTCCGACTGAGAGAGGAGC | 1620 |
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RESULT 9
LOCUS AY028416
DEFINITION Citrus x paradisi sodium/proton exchanger mRNA, complete cds.
ACCESSION AY028416
VERSION AY028416.2 GI:15812034
KEYWORDS Citrus x paradisi
SOURCE Citrus x paradisi
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eusids II; Sapindales; Rutaceae; Citrus.
REFERENCE 1 (bases 1 to 2135)
AUTHORS Porat,R., Povancello,D., Ben-Hayyim,G. and Lurie,S.
TITLE A heat treatment induced the expression of a Na+/H+ antiport gene
(JNHXL) in citrus fruit
JOURNAL Plant Sci. 162 (6), 957-963 (2002)
REFERENCE 2 (bases 1 to 600)
AUTHORS Porat,R., Lurie,S. and Povancello,D.
TITLE Direct Submission
JOURNAL Submitted (05-WAR-2001) Postharvest Sciences, ARO, The Volcani
Center, Bet Dagan 50250, Israel
REFERENCE 3 (bases 1 to 2135)
AUTHORS Porat,R., Lurie,S. and Povancello,D.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) Postharvest Sciences, ARO, The Volcani
Center, Bet Dagan 50250, Israel
REMARK Sequence update by submitter
COMMENT On Oct 1, 2001 this sequence version replaced gi:13509486.
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CDS

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[illegible]

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Db 2126 TCTGCTCAATGCAATGAGGTGGTGTGAACAGATCTCT 2164
RESULT 11
AY513732
LOCUS
DEFINITION
Medicago sativa Na+/H+ antiporter mRNA, complete cds.
ACCESSION
AY513732
VERSION
AY513732.1 GI:46250920
KEYWORDS
Medicago sativa
SOURCE
Medicago sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 1752)
An,B.Y. and Zhang,X.S.
Isolation and expression of MsNHX1 gene in alfalfa
Unpublished
JOURNAL
REFERENCE
2 (bases 1 to 1752)
An,B.Y. and Zhang,X.S.
Direct Submission
JOURNAL
Submitted (27-DEC-2003) College of Life Sciences, Shandong
Agricultural University, Daizong Street, Taian, Shandong 271018,
P.R. China
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 39.4%; Score 858; DB 8; Length 1752;
Best Local Similarity 72.0%; Pred. No. 4.2e-181;
Matches 1148; Conservative 0; Mismatches 440; Indels 6; Gaps 2;
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Qy 410 AGAATAGATGGATGAACGAATCCATCACCGCCTTGTGATTGGGCTAGGCACTGGTTTA 469

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ORIGIN

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RESULT 12
AY456096
LOCUS Medicago sativa Na+/H+ antiporter mRNA linear PLN 23-NOV-2003
DEFINITION Medicago sativa Na+/H+ antiporter mRNA, complete cds.
ACCESSION AY456096
VERSION AY456096.1 GI:38373524
KEYWORDS
SOURCE Medicago sativa
ORGANISM Medicago sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 2232)
Yang,Q.C., Wu,M.S. and Wang,P.Q.
The gene encoding Na+/H+ antiporter cloned from alfalfa
Unpublished
REFERENCE
2 (bases 1 to 2232)
Yang,Q.C., Wu,M.S. and Wang,P.Q.
Direct Submission
Submitted (01-NOV-2003) Turf & Forage Science, Chinese Academy of
Agricultural Science (CAAS), No.2 Yuanmingyuan West Road, Haidin,
Beijing 100094, China
FEATURES
Location/Qualifiers
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| Best Local Similarity | 72.0%; | Pred. No. 4.le-181; | | | |
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| QY | 350 | CGTTGAATCTCTTTGTTGCACTCTCTTTGCTGCTGTTATTTCTTGGTCATCTTTTGGAG | 409 | | |
| Db | 409 | CTATGAATCTGTTTGTGGCACTCTCTGTGCTGTTATTTGCTTGGTCATCTCTCTCGAGG | 468 | | |
| QY | 410 | AGATAGATGATGAAGCAATCCATCACCGCTTTGTTGATTTGGCTAGGCACCTGGTGTTA | 469 | | |
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| Db | 529 | TGATTTTGTCTGTTTGTGCTGTTGGAAGAAAGTTTCGATATTTCTTTTTCAGTGAAGATCTTT | 588 | | |
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| QY | 650 | GCACATCATATCTTAGTGTGAACACAGTCTTTTAAAGAGTTGGACATTTGGAACCTTTG | 709 | | |
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| Db | 829 | TGCAGGTTCTGAATCAAGATGACACCTTTTATTTGTATAGTCTTTGTTGGGAAGGTG | 888 | | |
| QY | 830 | TTCTGAATGATCAAGCTAGTGTGTTGCTTCAACCGGATTCAGACTTTGATCTCACTC | 889 | | |
| Db | 889 | TTGTGAATGATGCTACTCTAGTGGTCTTTTCAATGCAATTTCAAGCTTTGATCTTAACC | 948 | | |
| QY | 890 | ACCTAAACCAAGAGTCTCTTTTCACTCTCTTGGAACTCTTGTATTTGTTCTCTAA | 949 | | |
| Db | 949 | AACTGAACCTTCAATTTGCAATTCATTTCTTGGCACTCTCTGATTTTGTGTAGCAA | 1008 | | |
| QY | 950 | GTAACCTTGTGTGCTGCAACCGGCTCTGATAGTGGTATGTTATCAAGAAAGCTATACT | 1009 | | |
| Db | 1009 | GCACACTCTTGTGGCTTTGTGACAGGCTCTGCTCAGTGCCTATGTTATTAAGAAAGCTGACA | 1068 | | |
| QY | 1010 | TTGGAAGGCACCTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTTCTT | 1069 | | |
| Db | 1069 | TTGGCAGGCACCTCCACAGATCGTGGAGTGTCTTTATGATGCTTAATGGCATACCTCTCT | 1128 | | |
| QY | 1070 | ATATGCTTGTGAGCTTTTTCGACTTGGAGCGGTATCTCTACTGTGTTTTCTGTGGTATG | 1129 | | |
| Db | 1129 | ATATGCTGCTGAGTTAACTATCTGAGTGGCACTTTACCGTATTTCTTTTGTGGTATG | 1188 | | |
| QY | 1130 | TGATGTCCATTTACATGCGCAATGTTAAACGAGAGCTCAAGATTAACAAAGCAATTA | 1189 | | |
| Db | 1189 | TTATGTCTCATATTACTTGGCATTAATGTGACGAGAGTTCAAGAAATCACTCAAGCAT | 1248 | | |
| QY | 1190 | CTTTTGCACATTTGCTCATTTCTTGGCGACATTTATTTTCTTGTATGTTGGAATGGATG | 1249 | | |
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| QY | 1250 | CCTTGACATTTGCAAGTGGAGATCCGTTGAGTGACACACCGGGAACATCGATCGCAGTGA | 1309 | | |
| Db | 1309 | CCCTGGACATTTGAAAATGGAAGTTTGTAGTAGTAGTCTCTGGAACATCTATAGCTGCAA | 1368 | | |
| QY | 1310 | GCTCAATCTTAATGGTCTGGTCTGTCATGTTGGAGAGCAGCGTTTGGTCTTTCCGTATCTG | 1369 | | |
| Db | 1369 | GTTCAATGTTGGTCTTAATCTCTTCTTGGAGAGCAGCGTTTGGTCTTTCCGTATCTG | 1428 | | |
| QY | 1370 | TTCATCTAATCTAGCCAAAGAAATCAAAGCGAGAAATCAACTTTTAACTATGCAAGTTG | 1429 | | |
| Db | 1429 | TCTTATCCAACTTGAATAAAAAATCAACATCAAGAGATTTTCTTTCAGACAGCAAGTTA | 1488 | | |
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| Db | 1489 | TCAATTTGGTGGTCTGGTCTTATGAGAGGTCGTGTTTCAATGGCACTTGGTATATCACT | 1548 | | |
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| Db | 1549 | TCACCATGTGCGGGGCATCTCACTACGTAGCAATGCAATCATGATTAACGACCACTCA | 1608 | | |
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| QY | 1667 | COATACATATCTTTTGTGGACCAAGACTCTGTTCAATTGAGCC---TTCAGGGAACCCACA | 1723 | | |
| Db | 1729 | CATTCAATTTGCCACTTCTAGGAGATTTCCGAGATTTCTGAGCTGATCTTGAAGCCATG | 1788 | | |
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| Db | 1789 | AAATTCACCGACCGAACAGCCTTCGTCTTACTATCAACTCCAACTCACACTGTTCTATC | 1848 | | |
| QY | 1784 | ACTACTGAGACAAATTTGATGACTCTCTTCATGCGACCGCTCTTTGGAGGTCGTGGCTTTG | 1843 | | |
| Db | 1849 | GATTAAGCGGAAGTTTGATGATTCATTCATGCTGCTCTGTTTGTGTCGAGAGTTTG | 1908 | | |
| QY | 1844 | TACCCCTTTTCCAGGTTCTCCAACTGAGAGAAA | 1877 | | |
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| AY371319 | | | | | |
| LOCUS | AY371319 | 1656 bp | mRNA | linear | PLN 10-SEP-2003 |
| DEFINITION | Chenopodium glaucum Na+/H+ antiporter (NHX) mRNA, complete cds. | | | | |
| ACCESSION | AY371319 | | | | |
| VERSION | AY371319.1 | GI:34484303 | | | |
| KEYWORDS | mitochondrion | Chenopodium glaucum | | | |
| SOURCE | Chenopodium glaucum | | | | |
| ORGANISM | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Chenopodium. | | | | |
| REFERENCE | 1 (bases 1 to 1656) | | | | |
| AUTHORS | Li, J., Zhang, F., Ma, J., Cai, L. and Wang, Y. | | | | |
| TITLE | Using RT-PCR to Amplify the NHX Gene Fragment in Chenopodium glaucum | | | | |
| JOURNAL | Unpublished | | | | |
| REFERENCE | 2 (bases 1 to 1656) | | | | |
| AUTHORS | Zhang, F., Li, J., Ma, J., Cai, L. and Wang, Y. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (20-AUG-2003) College of Life Science and Technology, Xinjiang University, 14 Shengli Road, Urumqi, Xinjiang 830046, China | | | | |
| FEATURES | Location/Qualifiers | | | | |
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PN JP 2000157287-A/1
PD 13-JUN-2000
PF 16-SEP-1999 JP 1999261606
PR MARIKO SHONO, TAKAHIKO HAYAKAWA, AKIRA TANAKA
PC C12N15/09, A01H5/00, C07K14/415, C12Q1/68//C12N5/10, C12N15/00, PC
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CC
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Best Local Similarity 71.9%; Pred. No. 1.8e-175;
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DB 110 GTATCGTAATTGGTCACTCTTAGAGGAGAAATCGTTGGATGAATGATCTCAGTGCCT 169
QY 443 TGTGATTTGGCTAGGCACTGGTGTACCAATTTGTTGATTAGTAAGAGAAAAGCTTCG 502
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DB 1430 AAGATTATGAATTTGATGTTGGAAACCGAAACCATGAAGACACCACTGAGCGCGGACTA 1489
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RESULT 15

E63047

LOCUS

E63047 Na+/H+ antiporter protein and gene encoding it. linear 1668 bp DNA PAT 31-JAN-2002

DEFINITION

E63047

ACCESSION

E63047.1

VERSION

JP 2000157287-A/2.

KEYWORDS

unidentified

SOURCE

unclassified

ORGANISM

1 (bases 1 to 1668)

AUTHORS

Shono, M., Hayakawa, T. and Tanaka, A.

TITLE

Na+/H+ antiporter protein and gene encoding it

PATENT: JP 2000157287-A 2 13-JUN-2000;

PLANTECH RESEARCH INSTITUTE

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| COMMENT | OS | Atliplex gmelini | |
| | PN | JP 2000157287-A/2 | |
| | PD | 13-JUN-2000 | |
| | PF | 16-SEP-1999 JP 1999261606 | |
| | PI | MARIKO SHONO, TAKAHIKO HAYAKAWA, AKIRA TANAKA | |
| | PC | C12N15/09, A01H5/00, C07K14/415, C12Q1/68/12N15/10, C12N15/00, PC | |
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| QY | 383 | GTATTGCTTCTGCTCATCTTTTGGAAAGAGAAATAGATGGATGAACGAATCCATCACCGCCT | 442 |
| DB | 110 | GTATCGTAATTTGCTCATCTCTAGAGAGAGATCGTTGGATGATGATGATCCATCAGTCC | 169 |
| QY | 443 | TGTTGATTTGGGCTAGCAGCTGCTGTTTACCAATTTTGTGATTTAGTAAGGAAAGTCTGC | 502 |
| DB | 170 | TTCTTATAGCTTTGGCTACTGCGGTTGTGATCTCTGCTGATGTTAGTGAGGAAAGTTTCA | 229 |
| QY | 503 | ATCTTCTGCTTTAGTGAAGATCTTTTCTTCAATATATCTTTTGGCAGCCATTTATTTCA | 562 |
| DB | 230 | ATCTTTTGGCTTTCAGTGAAGATCTTTTCTTCAATATACCTTCTTCCACCGATTTATTTCA | 289 |
| QY | 563 | ATGCGGGTTTCAAGTAAAGAAAGACAGTTTTTTCGCAATTTTCGTGACTATTATGCTTT | 622 |
| DB | 290 | ATGCGGCTTTAGGTGAAGAGAGAGAGGTTCTTCCGCAACTTATTAATTTGTTATGT | 349 |
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| DB | 410 | TTAAGAAATTTGGATATTTGGTACTCTGGAGTTGGCAGACTATCTTGCATTTGGTGAAT | 469 |
| QY | 743 | TTGCTGCAACAGATTCAGTATGATACAGCTGAGGTTCTGAAATCAAGACGAGACACCTTTGC | 802 |
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Search completed: April 26, 2005, 06:38:39

Job time : 9545 secs

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| Qy | 61 | AGCTTCCAAATATTTTGAATTTTGATCTCTCGGGCTCTTTGTAAATCAGACTCAAGATAT | 120 |
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| ; APPLICANT: Blumwald, Eduardo | | | | | | | | | |
| ; TITLE OF INVENTION: SALT TOLERANT OIL CROPS | | | | | | | | | |
| ; FILE REFERENCE: 52964200500 | | | | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/10/617,624 | | | | | | | | | |
| ; CURRENT FILING DATE: 2003-07-10 | | | | | | | | | |
| ; PRIOR APPLICATION NUMBER: US 60/395,656 | | | | | | | | | |
| ; PRIOR FILING DATE: 2002-07-12 | | | | | | | | | |
| ; NUMBER OF SEQ ID NOS: 38 | | | | | | | | | |
| ; SOFTWARE: FastSeq for Windows Version 4.0 | | | | | | | | | |
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| ; TYPE: DNA | | | | | | | | | |
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| Db | 61 | AGCTTCCAAAATTTGAAATTTGATCTTCTGGCTCTTTTGTAAATCAGACTGAAGATAT | 120 | | | | | | |
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| Db | 421 | ATGAACGAATCCATACCCGCTTGTGATTTGGCTAGGCACTGGTGTACCAATTTGTTG | 480 | | | | | | |
| Qy | 481 | ATTAGTAAAGGAAAGAGCTCGCATCTTCTGCTTTTAGTGAAGATCTTTTTCATATAT | 540 | | | | | | |
| Db | 481 | ATTAGTAAAGGAAAGAGCTCGCATCTTCTGCTTTTAGTGAAGATCTTTTTCATATAT | 540 | | | | | | |
| Qy | 541 | CTTTTGCCACCCATATATTTCAATGAGAGGTTTCAAGTAAAGAGAGAGAGGTTTTCGCG | 600 | | | | | | |
| Db | 541 | CTTTTGCCACCCATATATTTCAATGAGAGGTTTCAAGTAAAGAGAGAGAGGTTTTCGCG | 600 | | | | | | |
| Qy | 601 | AATTTGCTGACTATTAATGCTTTTGGTGTGTTGGGACTATTATTCTTGGCAATCATATA | 660 | | | | | | |
| Db | 601 | AATTTGCTGACTATTAATGCTTTTGGTGTGTTGGGACTATTATTCTTGGCAATCATATA | 660 | | | | | | |
| Qy | 661 | TCTCTAGGTGTAACACAGTTCTTAAAGAGTTGGACATTTGGACCTTTCAGCTGGGTGAT | 720 | | | | | | |
| Db | 661 | TCTCTAGGTGTAACACAGTTCTTAAAGAGTTGGACATTTGGACCTTTCAGCTGGGTGAT | 720 | | | | | | |
| Qy | 721 | TATCTTGTCTATTGGTGCATATTGTCGAAAGATTCAGTATGATACCTGACAGGTTCTG | 780 | | | | | | |
| Db | 721 | TATCTTGTCTATTGGTGCATATTGTCGAAAGATTCAGTATGATACCTGACAGGTTCTG | 780 | | | | | | |
| Qy | 781 | AATCAAGACGAGACCTTTGCTTTTACAGTCTTGTGATTCGGAGAGGGTGTGTGAATGAT | 840 | | | | | | |
| Db | 781 | AATCAAGACGAGACCTTTGCTTTTACAGTCTTGTGATTCGGAGAGGGTGTGTGAATGAT | 840 | | | | | | |

| | | | |
|----|------|---|------|
| Db | 781 | AATCAAGACGAGACCTTTGCTTTTACAGTCTTGTGATTCGGAGAGGGTGTGTGAATGAT | 840 |
| Qy | 841 | GCAACGTCAGTTGTGTCTTCAACGCGATTCAAGAGCTTTGATCTCACTCACTAAACCCAC | 900 |
| Db | 841 | GCAACGTCAGTTGTGTCTTCAACGCGATTCAAGAGCTTTGATCTCACTCACTAAACCCAC | 900 |
| Qy | 901 | GAAGCTGCTTTTCACTCTTCTGAAACCTTCTTGTATTTGTTTCTCTAAGTACCTTGCTT | 960 |
| Db | 901 | GAAGCTGCTTTTCACTCTTCTGAAACCTTCTTGTATTTGTTTCTCTAAGTACCTTGCTT | 960 |
| Qy | 961 | GGTGTCTGCAACCGGCTCTGATAGTGGTATTTATCAAGAGCTATACCTTTGGAAGGCAC | 1020 |
| Db | 961 | GGTGTCTGCAACCGGCTCTGATAGTGGTATTTATCAAGAGCTATACCTTTGGAAGGCAC | 1020 |
| Qy | 1021 | TCAACTGACCGAGAGGTTGCCCTTATGATGCTTTATGGCGTATCTTTCTTATATGCTT | 1080 |
| Db | 1021 | TCAACTGACCGAGAGGTTGCCCTTATGATGCTTTATGGCGTATCTTTCTTATATGCTT | 1080 |
| Qy | 1081 | GAGCTTTTTCGACTTGAAGCGGTTATCTCACTGTGTTTCTCTGTGGTATTTGATGTCCT | 1140 |
| Db | 1081 | GAGCTTTTTCGACTTGAAGCGGTTATCTCACTGTGTTTCTCTGTGGTATTTGATGTCCT | 1140 |
| Qy | 1141 | TACACATGSCACAATGTAACGAGAGCTCAAGAAATAACAACAAGCATACCTTTGCAACT | 1200 |
| Db | 1141 | TACACATGSCACAATGTAACGAGAGCTCAAGAAATAACAACAAGCATACCTTTGCAACT | 1200 |
| Qy | 1201 | TTGTCAATTTCTTCCGAGAGACATTTATTTTCTTGTATTTGGAATGGATGCTTGGACAT | 1260 |
| Db | 1201 | TTGTCAATTTCTTCCGAGAGACATTTATTTTCTTGTATTTGGAATGGATGCTTGGACAT | 1260 |
| Qy | 1261 | GACAGTGAGATTCGCTGATGACACACCGGGAACATTCGATCGCAGTACGATCAATCCTA | 1320 |
| Db | 1261 | GACAGTGAGATTCGCTGATGACACACCGGGAACATTCGATCGCAGTACGATCAATCCTA | 1320 |
| Qy | 1321 | ATGGGCTGTGCTCATGTTGGAAGAGCAGGTTCTCTTTCGTTATCGTTTCTATCTAAC | 1380 |
| Db | 1321 | ATGGGCTGTGCTCATGTTGGAAGAGCAGGTTCTCTTTCGTTATCGTTTCTATCTAAC | 1380 |
| Qy | 1381 | TTAGCCAAAGAAATCAAAAGCGAGAGAAATCAAACTTTAACATGCAAGTTGTGATTTGGT | 1440 |
| Db | 1381 | TTAGCCAAAGAAATCAAAAGCGAGAGAAATCAAACTTTAACATGCAAGTTGTGATTTGGT | 1440 |
| Qy | 1441 | TCGTGCTCATGAGAGGTCGTATCTATGGCTCTTGGCTATACAAAGTTTACAAGGGCC | 1500 |
| Db | 1441 | TCGTGCTCATGAGAGGTCGTATCTATGGCTCTTGGCTATACAAAGTTTACAAGGGCC | 1500 |
| Qy | 1501 | GGGCAACAGATGTAACGCGGAATCAATCATGATCAGGATCAGTAACTGTCTGCTT | 1560 |
| Db | 1501 | GGGCAACAGATGTAACGCGGAATCAATCATGATCAGGATCAGTAACTGTCTGCTT | 1560 |
| Qy | 1561 | TTTAGCACAGTGTGTTTGGTATGCTGACCAAAACCACTCATAGCTTACCTATTACCGCAC | 1620 |
| Db | 1561 | TTTAGCACAGTGTGTTTGGTATGCTGACCAAAACCACTCATAGCTTACCTATTACCGCAC | 1620 |
| Qy | 1621 | CAGAACGCCACCAACGAGATGTTATCTGATGACACACCCCAAAATCCATATATCCCT | 1680 |
| Db | 1621 | CAGAACGCCACCAACGAGATGTTATCTGATGACACACCCCAAAATCCATATATCCCT | 1680 |
| Qy | 1681 | TTGTTGGACCAAGACTCGTTTCAATGAGCTTCAGGGAACCAATGTGCTCGGCTGAC | 1740 |
| Db | 1681 | TTGTTGGACCAAGACTCGTTTCAATGAGCTTCAGGGAACCAATGTGCTCGGCTGAC | 1740 |
| Qy | 1741 | AGTATACGTGGCTTCTTGACACGGCCACTCGAAACCGTGCATTTACTTACGGAGACAATTT | 1800 |
| Db | 1741 | AGTATACGTGGCTTCTTGACACGGCCACTCGAAACCGTGCATTTACTTACGGAGACAATTT | 1800 |
| Qy | 1801 | GATGACTCTTTCATGCGACCCGCTTCTTGGAGGTCGTGGCTTTGTACCCCTTTGTCCAGGT | 1860 |
| Db | 1801 | GATGACTCTTTCATGCGACCCGCTTCTTGGAGGTCGTGGCTTTGTACCCCTTTGTCCAGGT | 1860 |
| Qy | 1861 | TCTCCAACTGAGAGAAACCTCTCTGATCTTAGTATAGGCTTGGGGTAAAGTGAAGAAA | 1920 |
| Db | 1861 | TCTCCAACTGAGAGAAACCTCTCTGATCTTAGTATAGGCTTGGGGTAAAGTGAAGAAA | 1920 |


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Db 1381 TCCATACATATCCCTTTGTTGACCAAGACTCGTTCAATGAGCCTTCAGGGAACCAAT 1440
Qy 1726 GTGCCTCGGCTGACAGTATACGTGGCTTCTTGACACGGCCCACTCGAAACCGTGCAATTAC 1785
Db 1441 GTGCCTCGGCTGACAGTATACGTGGCTTCTTGACACGGCCCACTCGAACCGTGCAATTAC 1500
Qy 1786 TACTGAGACAAATTGATGACTCCTTCATCGGACCGCTCTTTGGAGGTCGTGGCTTTGTA 1845
Db 1501 TACTGAGACAAATTGATGACTCCTTCATCGGACCGCTCTTTGGAGGTCGTGGCTTTGTA 1560
Qy 1846 CCCTTTGTTCCAGGTTCTCAACTGAGAGAAACCTCCCTGATCTTAGTAAGGCTTGA 1902
Db 1561 CCCTTTGTTCCAGGTTCTCAACTGAGAGAAACCTCCCTGATCTTAGTAAGGCTTGA 1617

RESULT 4
US-09-938-842A-1239
; Sequence 1239, Application US/09938842A
; Publication No. US2004009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepis, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1239
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1239

Query Match 74.2%; Score 1617; DB 11; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 286 ATGTTGGATTCTCTAGTGTGAACTGCCTTCGTTATCGACATCTGATCAGGCTTCTGTG 345
Db 1 ATGTTGGATTCTCTAGTGTGAACTGCCTTCGTTATCGACATCTGATCAGGCTTCTGTG 60

Qy 346 GTTGGCTTGAATCTCTTTGTTGCACTTCTTTGTTGCTTGTATGTTCTTGTGTCATCTTTTG 405
Db 61 GTTGGCTTGAATCTCTTTGTTGCACTTCTTTGTTGCTTGTATGTTCTTGTGTCATCTTTTG 120

Qy 406 GAAGAGAATAGATGAGTGAACGAATCCATCAGCCCTTGTGATTTGGGCTAGGCACTGGT 465
Db 121 GAAGAGAATAGATGAGTGAACGAATCCATCAGCCCTTGTGATTTGGGCTAGGCACTGGT 180

Qy 466 GTTACCAATTTGTTGATTAGTAAGGAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT 525
Db 181 GTTACCAATTTGTTGATTAGTAAGGAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT 240

Qy 526 CTTTTCTTCATATATCTTTTGGCAACCCATTTATTCATGACGGTTTCAAGTAAAAAAG 585
Db 241 CTTTTCTTCATATATCTTTTGGCAACCCATTTATTCATGACGGTTTCAAGTAAAAAAG 300

Qy 586 AAGCAGTTTTTCCGCAATTTCTGACTATTTATGCTTTTTTGGTGTGTTGGGACTATTATT 645
Db 301 AAGCAGTTTTTCCGCAATTTCTGACTATTTATGCTTTTTTGGTGTGTTGGGACTATTATT 360

Qy 646 TCTTGCACAATATATCTCTAGGTGTAAACAGTTCTTTAAGAAAGTTGGACATTTGAACC 705
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Db 361 TCTTGCACAATCATATCTCTAGGTGTAAACAGTTCTTTAAGAAAGTTGGACATTTGAACC 420
Qy 706 TTTGACTTTGGTGCAATATATCTTGTATTTGGTGCATATTTGCTGCAACAGATTCAGTATGT 765
Db 421 TTTGACTTTGGTGCAATATATCTTGTATTTGGTGCATATTTGCTGCAACAGATTCAGTATGT 480
Qy 766 AACTGCAAGTTCTGNAATCAAGACGAGACACCTTTGCTTTACAGTCTTGTATTCGGAGAG 825
Db 481 AACTGCAAGTTCTGNAATCAAGACGAGACACCTTTGCTTTACAGTCTTGTATTCGGAGAG 540
Qy 826 GGTGTTGTGAATGATGATCAACAGTTCAGTTGTGTTCTTCAAGCGGATTCAGAGCTTTGATCTC 885
Db 541 GGTGTTGTGAATGATGATCAACAGTTCAGTTGTGTTCTTCAAGCGGATTCAGAGCTTTGATCTC 600
Qy 886 ACTCACTAAACCAACGAGCTGCTTTTCATCTTCTTTGGAAACTTCTTTGATTTGTTTCTC 945
Db 601 ACTCACTAAACCAACGAGCTGCTTTTCATCTTCTTTGGAAACTTCTTTGATTTGTTTCTC 660
Qy 946 CTAAGTACCTTGTGTTGCTGCAACCGGTCTGATAAGTGCGGTATCTTATCAAGAAAGCTA 1005
Db 661 CTAAGTACCTTGTGTTGCTGCAACCGGTCTGATAAGTGCGGTATCTTATCAAGAAAGCTA 720
Qy 1006 TACTTTGGAAGGCACCTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGGCTATCTT 1065
Db 721 TACTTTGGAAGGCACCTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGGCTATCTT 780
Qy 1066 TCTTATATCTTGTGCTGAGCTTTTCGACTTTGAGCGGTATCTCTACTGTGTTTCTGTGGT 1125
Db 781 TCTTATATCTTGTGCTGAGCTTTTCGACTTTGAGCGGTATCTCTACTGTGTTTCTGTGGT 840
Qy 1126 ATTGTGATGCTCCCATTTACACATGCGGCAATGTAACGGAGAGCTCAAGAAATCAACAAAG 1185
Db 841 ATTGTGATGCTCCCATTTACACATGCGGCAATGTAACGGAGAGCTCAAGAAATCAACAAAG 900
Qy 1186 CATACCTTTGCAACTTTTGTCTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 1245
Db 901 CATACCTTTGCAACTTTTGTCTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 960
Qy 1246 GATGCTTGGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305
Db 961 GATGCTTGGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020
Qy 1306 GTGAGCTCAATCTTAATGGGCTGTGTCATGTTTGAAGAGCAGCGTTCGTTTCCGTTA 1365
Db 1021 GTGAGCTCAATCTTAATGGGCTGTGTCATGTTTGAAGAGCAGCGTTCGTTTCCGTTA 1080
Qy 1366 TCGTTTCTATCTAACTTTAGCAGAGAAATCAAGCGAGAAATCAACTTTTAACATGCGAG 1425
Db 1081 TCGTTTCTATCTAACTTTAGCAGAGAAATCAAGCGAGAAATCAACTTTTAACATGCGAG 1140
Qy 1426 GTTGTGATTTGGTGTCTGCTCTCATGAGAGGTGCTGATCTATATGCTCTTTGCATACAAC 1485
Db 1141 GTTGTGATTTGGTGTCTGCTCTCATGAGAGGTGCTGATCTATGCTCTTTGCATACAAC 1200
Qy 1486 AGTTTACAAGGGCGGGGACACAGATGTACGGGGAATGCAATCATGATCAGAGTACG 1545
Db 1201 AGTTTACAAGGGCGGGGACACAGATGTACGGGGAATGCAATCATGATCAGAGTACG 1260
Qy 1546 ATAACCTGTCTGCTTTTGTAGCAGTGTGTTTGTGATGCTGACCAAAACCACTCATAAGC 1605
Db 1261 ATAACCTGTCTGCTTTTGTAGCAGTGTGTTTGTGATGCTGACCAAAACCACTCATAAGC 1320
Qy 1606 TACTATTACCGCACAGAACCGCACACGAGCATGTTATCTGATGACAAACACCCCAAAA 1665
Db 1321 TACTATTACCGCACAGAACCGCACACGAGCATGTTATCTGATGACAAACACCCCAAAA 1380
Qy 1666 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTCATTGAGCGCTTCAGGGAACCAAT 1725
Db 1381 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTCATTGAGCGCTTCAGGGAACCAAT 1440
Qy 1726 GTGCTTCGGCTGACAGTATAGTGGCTTCTTGACACGGCCCACTCGAACCGGTGCAATTAC 1785
Db 1441 GTGCTTCGGCTGACAGTATAGTGGCTTCTTGACACGGCCCACTCGAACCGGTGCAATTAC 1500
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Qy 1786 TACTGGAGACAAATTGTAGTACTCTTTCATGCGACCCGCTCTTTGAGGTCGTGGCTTTGTA 1845
Db 1501 TACTGGAGACAAATTGTAGTACTCTTTCATGCGACCCGCTCTTTGAGGTCGTGGCTTTGTA 1560
Qy 1846 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCCGTCATCTTAGTAAGGCTTGA 1902
Db 1561 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCCGTCATCTTAGTAAGGCTTGA 1617

RESULT 5
US-10-155-535-1
; Sequence 1, Application US/10155535
; Publication No. US20030046729A1
; GENERAL INFORMATION:
; APPLICANT: Blumwald, Eduardo
; APPLICANT: Apose, Maris
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
; TITLE OF INVENTION: EXPRESSION OF VACUOLAR CATION-PROTON ANTIPORTERS
; FILE REFERENCE: 529152000720
; CURRENT APPLICATION NUMBER: US/10/155,535
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/271,584
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,474
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: 60/116,111
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FAST-SEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-155-535-1

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| | | | |
|----|------|--|------|
| Db | 833 | CGACTCTGTATGACACACTACAGGTTCTCAATCAAGATGAGACACCTTTGCTTTTACAGTC | 892 |
| Qy | 812 | TTGTATTCCGAGAGGGGTGTGTAATGATGCAACGTCAGTTGTGTGCTTCTCAACCGCATTCT | 871 |
| Db | 893 | TTGTATTGGAGAGGGCGTTGTGAATGATGCCAATCTGTTGTGCTCTTCAATGCTATTCT | 952 |
| Qy | 872 | AGAGCTTTGATCTCACTCAACCAAGAGCTGCTTTTTCATCTCTTTGGAAACTTCT | 931 |
| Db | 953 | AGAGTTTGGACCTCACCACCTTAACCATGAAGCAGCTTTTCAATTTCTTTGGAACTTTT | 1012 |
| Qy | 932 | TGTAATTTGTTTCTCCTAAGTACCTTGTCTGCTGCTCAACCGCTCTGTAAAGTGCCTATG | 991 |
| Db | 1013 | TTTAATCTGTTTCTCTTGAGCACCGGACTTGGTGTGCGCACTGTGCTGTAAAGTGCCTATG | 1072 |
| Qy | 992 | TTATCAAGAAGCTATACCTTTTGGAAGGCACCTCAACTGACCGAGAGGTTGGCCCTTATGATGC | 1051 |
| Db | 1073 | TCATCAAGAACTGTAATTTTGGAAGGCACCTCGACTGATCGAGAAGTTGGCCCTCATGATGC | 1132 |
| Qy | 1052 | TTATGGCGTATCTTTCTTATATGCTTGTCTGAGCTTTTTCGACTTGTAGCGGTATCCTCACTG | 1111 |
| Db | 1133 | TTATGGCTTATCTTTTTCATATATGCTTGTCTGAGCTATTCGCTTTGTAGTGTATCCTAACTG | 1192 |
| Qy | 1112 | TGTTTTTCTGTGGTATTGTGATGTCCCATPACATGCGACAAATGTAAACGGAGAGCTCAA | 1171 |
| Db | 1193 | TATTTTCTGTGGATTGTGATGTCCCATPACACTTGGCACATGTCAACGAGAGCTCAA | 1252 |
| Qy | 1172 | GAATPACAAAGCATACCTTTTGCAACTTTGTCTATTTCTTGGGAGACATTTATTTTCT | 1231 |
| Db | 1253 | GAATTACTACCAAGCATGCCCTTTGTCTACTTTGTCTGTTCTCGCTGAGACTTTTATTTTCC | 1312 |
| Qy | 1232 | TGTATGTTGGAATGGATCTCGACATTTGACAAGTGGAGATCCGTGTAGTGTACACACCGG | 1291 |
| Db | 1313 | TCTACGTTGGAAATGGATGCAATGGACATAGAGAAATGGAGATTCGTGTAGTGTACAGCCCG | 1372 |
| Qy | 1292 | GAAATCGATGCGATGAGCTCAATCCTAATGGCTCTGGTCTGTGTTGGAAGACGAGCT | 1351 |
| Db | 1373 | GGACATCAGTTGCACTGAGCTCAATTTCTAATGGCTCTAGTCTGCTTGTGAAGACGAGCTT | 1432 |
| Qy | 1352 | TCGCTCTTCCGTTATCGTTTCTATCTAACTTAGCCCAAGAGATCAAGCGAGAAATCA | 1411 |
| Db | 1433 | TTGTCTTTCTCTTTCTTATCAAACTTAGCCCAAGAGATCAAGCGAGAAATCA | 1492 |
| Qy | 1412 | ACTTTAACATCGAGTTGTATTGGTGTCTGGTCTCATGAGAGGTGCTGTATCTATGG | 1471 |
| Db | 1493 | GCATCAAGCAGCAAGTTGTATCTGTGGCTGGTCTAATGAGAGGTGCTGTATCTATGG | 1552 |
| Qy | 1472 | CTCTTGATACACACAGTTTAAAGGGCCGGGACACAGATGTACCGGGATGTCAATCA | 1531 |
| Db | 1553 | CTCTTGCTTCAATAAAGTTTACAAGATCAAGGACACAGAAATTTGCGCGGAAATGCAATCA | 1612 |
| Qy | 1532 | TGATCAGAGTACGATAACTGTCTGTCTTTTATAGCACAGTGTGTTTGGTATGCTGTACCA | 1591 |
| Db | 1613 | TGATTACCAGTACAAATAACCGTCTGTCTTTTATAGCACCAATGTTTGGTATGCTAAACA | 1672 |
| Qy | 1592 | AACCATCTAAGCTTACTTATTAACCGCACAGAACGCT-----CACCAAGAGATGT | 1642 |
| Db | 1673 | AACCATCTGATTAGTACTTAATGCCACACCAAAAGCGACCACTGATGATGATGATGATG | 1732 |
| Qy | 1643 | TATCTGATGACACACCCCAAAATCCATACATATCCCTTTGTTGG-----ACCAAG | 1693 |
| Db | 1733 | TATCGAGATAGTACTCCGAATTAATCAATTCGCTCTCGATGGTGTGAACAGCTAG | 1792 |
| Qy | 1694 | ACTCGTTTCAATGAGCTTACAGGGAACCAAAATGTGCTCGGCTGTACAGTATACGTGGCT | 1753 |
| Db | 1793 | ATTCAATTTGAGTTTACCTGGGAGCCACAGGACGTGCCACGACCAAAAGCCTTCGAGGTT | 1852 |
| Qy | 1754 | TCTTGACAGGCCCACTCGNAACGTTGCAATTACTTGGAGACAAATTTGATGACTCTTCA | 1813 |
| Db | 1853 | TCCTCATGCGCCCAACAGGACTGTCCATTTACTTACGTGGAGACAGTTTGTATGATGCTTCA | 1912 |
| Qy | 1814 | TGCGAACCGCTTTTGGAGGTCTGTGGCTTTGTATACCTTTTGTTCAGAGTTCTTCAACTGAGA | 1873 |

| Accession | Gene | Strain | Accession | Gene | Strain |
|-----------|------|---|-----------|------|--------|
| D8 | 1913 | TGCGTCCTGTGTTTGGTGGTGGCGGATTCGTTCCCTTTGTCCTGGTTCTCCGACTGAGA | 1972 | | |
| Db | | | | | |
| Qy | 1874 | GAAACCCCTCCTGATCTTTAGTAAGCGCTTGAGGGTTAACGTGGAGAGAAAAGCTT | 1924 | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
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| | | | | | |
| Db | 1973 | GAAGACGCCATGATCTTTAGTATAACCTTTGAGGAGAGAAAGATATATAGAAAATCTT | 2023 | | |

RESULT 6

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US-10-425-114-20609
; Sequence 20609, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 20609
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3242-431-A12_FLI
US-10-425-114-20609

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|-----------------------|--------------|-----------|------------|-------|--------|------|
| Query Match | 38.4% | Score | 837.4 | DB 17 | Length | 1915 |
| Best Local Similarity | 71.2% | Pred. No. | 1.2e-196 | | | |
| Matches 1143 | Conservative | 0 | Mismatches | 441 | Indels | 21 |
| | | | | | Gaps | 2 |

| | | | |
|-----|----|--|-----|
| 294 | Qy | TTCTCTAGTGTGAAACGCTTCGTTATTCGACATCTGATCAGCCTCTCTGTGGTGTGGCTT | 353 |
| | | | |
| 2 | Db | TTCTGTGTTTCAAAATTTGCAACGTTATTCACACCTCAGACCACTCCGCTGCTCCAT | 61 |
| | | | |
| 354 | Qy | GAATCTCTTTGTTGTCACCTCTTTGTGCTGTGTTATTTGTTCTTGGTGCATCTTTTGGGAAGAGAA | 413 |
| | | | |
| 62 | Db | GAACCTTAATTTGTGGCACCTTTCTTTGTGGTGTGTTATTTGCTCTGGCCATCTTCTTGAGGAGAA | 121 |
| | | | |
| 414 | Qy | TAGATGGATGAACGAATCCATCACCGCCTGTTGATTGGGCTAGGCACCTGGTGTATCCAT | 473 |
| | | | |
| 122 | Db | TCGATGGATGAACGAGCTATCACTGCCCTTTGATTGGTGTTTGGCACTGSCGTAGTCAT | 181 |
| | | | |
| 474 | Qy | TTTGTGATTAGTAAAGAAAGAGCTCGCATCTTCTCGTCTTTTAGTGAAGATCTTTTCTT | 533 |
| | | | |
| 182 | Db | TTTGTCTTTTAGTGGTGGCAAAAGCTCACATATTTCTTGTTTTCAGTGAAGATCTTTTCTT | 241 |
| | | | |
| 534 | Qy | CATATATCTTTTGGCACCCATTAATATCAATGACGAGGTTTCAAGTAAAAAGAGACAGTT | 593 |
| | | | |
| 242 | Db | TATATATCTTCTACCACTTAATATCAATGCGCGGTTTCAGGTGAAAAGAGACAGTT | 301 |
| | | | |
| 594 | Qy | TTTCCGCAATTTCTGTGACTATATGCTTTTGGTGCTTGTGGGACTATATTTCTCTGCAC | 653 |
| | | | |
| 302 | Db | TTTTGTAACTTCATGACCATCATGTTGTTGGTGCTATTGGTACATTAATATCATGTAC | 361 |
| | | | |
| 654 | Qy | AATCATATCTAGGTGTAACACACAGTTCTTTAAGAAGTTGGACATTTGAACTTTTGACTT | 713 |
| | | | |
| 362 | Db | CATCATAACTTTGGGTGCCACACAAAATTTTAAAGAGGTTGGATGTTGCTCTCGGAATT | 421 |
| | | | |
| 714 | Qy | GGGTGATTATCTTGCTATTGGTGCATATTTGCTTGCAACAGATTTCAGTATGTACACTGCA | 773 |
| | | | |
| 422 | Db | AGGGGATTTCTTAGCAATTTGGTGGAAATATTTGCTTGCAACCGAATTTCTGTTGCAATTTGCA | 481 |
| | | | |
| 774 | Qy | GGTTCGTAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTAATTCGAGAGGGGTGTTGT | 833 |
| | | | |
| 482 | Db | GGTGCTAAATCAGAGTAGAGACACCTTTGCTGTACAGTCTTGTAATTTGGGAGGGGTGTTGT | 541 |
| | | | |
| 834 | Qy | GAATGATGCAACGTCAGTTGTGGTCTTTCAACCGAATTCAGAGCTTTGATCTCACTCACT | 893 |
| | | | |

RESULT 7

| | | | | |
|-----------------------|-----------------|---------------------|------------|--------------|
| Query Match | 37.7%; | Score 821.8; | DB 17; | Length 1968; |
| Best Local Similarity | 70.6%; | Pred. No. 9.1e-193; | | |
| Matches 1134; | Conservative 0; | Mismatches 452; | Indels 21; | Gaps 2; |

| | | | |
|----|-----|--|------|
| QY | 292 | GATTCTCTAGTGTGGAACAGCCTTCGTTATCGACATCTCATCACGCCTTCTCTGGTTGGG | 351 |
| Db | 16 | GGTCTGTGTTTCAAAATGCAAAAGGTATPCACCCTCGACCATCCCTCCGTGTGTCCTCC | 75 |
| QY | 352 | TTGAAATCTCTTTGTGTGCCACTTCTTTGTGCTGTATTGTTCTTGGTCATCTTTTGGAGAAG | 411 |
| Db | 76 | ATGAACCTATTATTGGGCACCTCTTTGTGGTGTATTATGTCTTGGCCANCTTCTTGAGGAG | 135 |
| QY | 412 | AATAGATGGATGAACGAATCCATCCGCCCTGTGTGATTGGGCTAGGCACTCGTGTATCC | 471 |
| Db | 136 | AATCGTGGATGAACGAGTCTATCACTGCTCTTTTGATTGGTGTGTGCACTGGCATATGTC | 195 |
| QY | 472 | ATTTTTGTTGATTAGTAAGAAGAAAAGCTCCGCACTTCTGCTCTTTTAGTGAAGATCTTTTC | 531 |
| Db | 196 | ATTTTGTGCTTTAGTGTGGCAAAGCTCCGCATATTCCTGTTCTTCACTGAAGATCTTTTC | 255 |
| QY | 532 | TTCATATATCTTTTGGCCACCCATTATATTCAATCGAGGGTTCCTCAAGTAAAAAAGAAGCAG | 591 |
| Db | 256 | TTTATATACCTTCTACCACTATAATATTAAIGCCGGTTCACGTTGAANAAGAAGCAG | 315 |
| QY | 592 | TTTTTCCGCAATTCGTGACATAATATGCTTTTTTGGTGTCTGTGGGACATATATTATTTCTTCG | 651 |
| Db | 316 | TTTTTTGTGTAACCTTCATGACCATCATGTCTGTTGGTGTCTATTGGTACATTAATATCATGT | 375 |
| QY | 652 | ACAATCATATCTCTAGGTGTAAACAGTCTCTTTAAGAAGTTCGACATTTGGAACCTTTTGCAC | 711 |
| Db | 376 | ACCATCATPACTTTGGGTGGCCACAAATTTTTTAAGAGGTGGATGTTGGTCTCTCTGGNA | 435 |
| QY | 712 | TTGGGTGAATATCTTGCTATTGGTGCCATATTTGCTGCAACAGATTCAGTATGTACACTG | 771 |
| Db | 436 | TTAGGGGATTTCTTAGCAAATTTGGTGCAATATTTGCTGCAACGSAITCTGTTTGACATTTG | 495 |
| QY | 772 | CAGGTTCTGAATCAAGACGAGACACCTTTGCTTTAACGTCTTGATATTCGGAAGGGTGT | 831 |
| Db | 496 | CAGGTGCTTAAATCAGSAGTGAACACCTTTGCTGTCAGTCTTGATATTTGGGAGGGTGT | 555 |
| QY | 832 | GTGAATGATGCAACGTCAGTTGTGCTTCCAACCGGATTCAGAGCTTTTGATCTCACTCAC | 891 |
| Db | 556 | GTGAATGATGCTACATCAGTGTGTGCTTTCAATGCAANTCAAAGCTTTGACCTCAACCA | 615 |
| QY | 892 | CTAAACCAACGAAGCTGCTTTTTCATCTCTTTGGAACTCTCTGATTTGTTTCTCTCAAGT | 951 |
| Db | 616 | ATTGACTCTTCAATTGCTGTACACTTTTTTGGGAAATTTCTTGATCTATTATTATTCGAAGC | 675 |
| QY | 952 | ACCTTGTCTGGTCTGCAACCGGTCTGAATGAGTGGGTATGTTATCAAGAAGCTATACATTT | 1011 |
| Db | 676 | ACAATGCTTGAGTTTTGAACAGGCTACTATAGTGTCTTACATTTATTTAAAGAAGCTGATATT | 735 |

APPLICANT: SWORDS, KATHY M. M.
; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0162
; CURRENT APPLICATION NUMBER: US/10/369,324
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-369-324-38

Query Match 36.68; Score 797.6; DB 17; Length 1620;
Best Local Similarity 69.38; Pred. No. 8.2e-187; Indels 3; Gaps 1;
Matches 1101; Conservative 0; Mismatches 484;

| | | | |
|----|------|--|------|
| Qy | 287 | TGTTGGATCTCTAGTGTGGAAGCTGCTTTCGTTATCGACATCTGTATCAGCGCTTCTGTGG | 346 |
| Db | 11 | TGCTGGCTTCTGTTTCCAAAGCTGGGCTTTTGGGTACTTCAGATCATGCTTCGTGG | 70 |
| Qy | 347 | TTGGTTGAATCTCTTGTGTGCACTTCTTGTGCTTGTATGTTTGTGGTCACTTTTGG | 406 |
| Db | 71 | TATCCATCAACCTCTTGTGGCACTCTTGTGCTTGTGCTATCATCATCATGTTGGTCACTCTTGG | 130 |
| Qy | 407 | AAGAGATAGATGATGAAGCAATCCATCCAGCTGCTTGTGATGTTGGCTAGGCACTGGTG | 466 |
| Db | 131 | AGAGAACCCGCTGGTAAATGAGTCCATTAATGCGCTTAAATGGTGTGTACAGGAG | 190 |
| Qy | 467 | TTACCAATTTTGTGATTAGTAAGAAAGAAAGCTGCACTCTTCTGCTTTAGTGAAGATC | 526 |
| Db | 191 | TGTTATCTTGTGTAAGTGTGGAAGAACTCACACCTTCTGTTTTCAGTGAAGATC | 250 |
| Qy | 527 | TTTCTTCAATATCTTTTGGCAACCCATTAATTAATGAGGGTTTCAAGTAAAAAGA | 586 |
| Db | 251 | TCCTTTTCAATATGATCTTCTTCCAAATCATATTTAATGAGGGTTTTCAGTAAAAAGA | 310 |
| Qy | 587 | AGCAGTTTTCGCAATTCGTGACATTAATGCTTTTGTGCTGTTGGCACTATATTT | 646 |
| Db | 311 | AGCAATTTTTCGTAACCTCTTACTATAATGATGTTTCGGAGCAATTTGGTACCCCTGCT | 370 |
| Qy | 647 | CTTGCAATATCATATCTTAGTGTAAACAGTTCTTTAAGAAAGTTGCAATTTGGAACCT | 706 |
| Db | 371 | CATGTGCATTAATCATTAAGTGAATTCAACTTTCAAGAAAGTTGCAATTTGAATTC | 430 |
| Qy | 707 | TTGACTTGGTGATTAATCTTGTCTATTTGGTCCATATTTGCTGCAACAGATTCAGTATGTA | 766 |
| Db | 431 | TAGATATTGGGATTAATCTTGGCAATTTGGAGCAATATTTGCTGCCACAGATTTCCGTCTGCA | 490 |
| Qy | 767 | CACGTGAGTTTGAATCAACAGAGACACCTTGTCTTTACAGTCTGTGATTCGGAGAGG | 826 |
| Db | 491 | CATTGCAAGTCTTACATCAGGATGAGACACCCCTCTTTACAGTCTGTGATTTGGAGAG | 550 |
| Qy | 827 | GTGTTGTAATGATGCAACCTGAGTTGTGTCTTCAACGGATTCAGAGCTTTGATCTCA | 886 |
| Db | 551 | GAGTTGTAATGATGATCAATCGTGTGCTTTTCAATGCTATTAACAACTTTGACCTTA | 610 |
| Qy | 887 | CTCACCTTAAACCAAGAGCTGCTTTTCACTCTTCTTGGAACTTCTTGTATTTGTCTCC | 946 |
| Db | 611 | CGAGCGTGAATCCAGTATAGCCCTCAGTTTCTTGGCAACTTCTTCTATCTGTCTCTTG | 670 |
| Qy | 947 | TAGTACCTTGTGCTGCTGCAACCGGTCTGATGATGAGTGGTATGTTATCAAGAGCTAT | 1006 |
| Db | 671 | CTAGCACTTTTACTGGGAGCAGGAACCTGCTTCTTCTAGTGTCTTACATTTATCAAGAGCTGT | 730 |
| Qy | 1007 | ACTTTGAGGCACTCAACTGACCGAGAGGTGCGCTTATGATGCTTATGCGCTATCTTT | 1066 |
| Db | 731 | ATTTTGGCAGCACTCACAGATCGTGAGGTGCGCTTATGATGCTCATGCTTACTTAT | 790 |

RESULT 9

US-10-607-538-38
; Sequence 38, Application US/10607538
; Publication No. US20040107455A1
; GENERAL INFORMATION:
; APPLICANT: ROMMENS, CAIUS
; APPLICANT: YE, JINGSONG
; APPLICANT: HUMABA, JAIME M.
; APPLICANT: YAN, HUA
; APPLICANT: SWORDS, KATHY
; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0167
; CURRENT APPLICATION NUMBER: US/10/607,538
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 10/369,324
; PRIOR FILING DATE: 2003-02-20

| | | | |
|----|------|---|------|
| Qy | 1067 | CTTATATGCTTGTGCTGAGCTTTTCGACTTGAGCGGTATCTCCTCAGCTGTGTTTCTGTGGTA | 1126 |
| Db | 791 | CATACATGCTGGCTGAATTTCTATTTGAGTGGGATTTCTCAGTGTATTTTCTGTGGTA | 850 |
| Qy | 1127 | TTCTGATGCCCATTAACATGCAATGCTAAGAGAGCTCAAGAGATTAACAAAGC | 1186 |
| Db | 851 | TTGTATGCTCATTAACATGCTGCAATGCTGAGAGATTAAGAGATTAACAAAGC | 910 |
| Qy | 1187 | ATACCTTTGCAACTTTGTCTATTTCTTGGGAGACATTTATTTTCTGTATGTTGGAATGG | 1246 |
| Db | 911 | ACGCTTTTGCACACTTTGTCTATTTCTTGGGAGACATTTTCTCTCTCTATGTCGCGATGG | 970 |
| Qy | 1247 | ATGCTTTGACATTTGACAGTGGAGATCGGTGATGACACACCGGGAACATCGATCCAG | 1306 |
| Db | 971 | ATGCTTTTGGATATCGAGAAAGTGGAAATTTGTGTCGACAGCGCTGGATTAATCAATTTCCG | 1030 |
| Qy | 1307 | TGAGCTCAATCCTAATGGGTCTGGTCTATGTTGGAAGAGCAGGTTCGTCTTTCCTGGTAT | 1366 |
| Db | 1031 | TGAGTTCAATCTGATGGGATTAATCTTGTCTGGGAGAGCTGCTTGTGTTTTCATTTAT | 1090 |
| Qy | 1367 | CGTTTCTATCTAATTTAGCCAAAGAAATCAAGCGGAGAAATCAACTTTTAAACATGCGG | 1426 |
| Db | 1091 | CATTCTTCTCAACTTAATGAAGAAATCTCGGAGCAAAAATTTACCTTTAGGCGAGCAAG | 1150 |
| Qy | 1427 | TTGTGATTTGGTGGTCTGCTCTCATGAGAGTCTGTATCTATGCTTGTGCTTTCGATACACA | 1486 |
| Db | 1151 | TGATAATATGTTGGGAGGTTTGTATGAGAGGCGAGTGTCCATGCGCACTGGCATATAATA | 1210 |
| Qy | 1487 | AGTTTACAGGGCGGGGACACACAGATGTACCGGGGAATGCAATCATGATCACGAGTACGA | 1546 |
| Db | 1211 | AGTTCTCTGTTGGGGACACACTCAACTGCGAGCAATGCATTAATGATTAACGACGACGA | 1270 |
| Qy | 1547 | TAACTCTCTCTTTTAGCACAGTGGTGTGTTGTTGTTGCTGACCAACCACTCATAGCT | 1606 |
| Db | 1271 | TAAACATTTCTTATTTTACGACCAATGTTTTCGTTTAAATGACAAAACCTTTATAGTC | 1330 |
| Qy | 1607 | ACCTATTACGGACCAAGAGCGCCACACGAGCATGTTATCTGATGACACACCCCAAAAT | 1666 |
| Db | 1331 | TCCTGCTGCCACACAGAGGCAATTTGATGACAGTGTATCAGGTGCAAAATCTCCAAAGT | 1390 |
| Qy | 1667 | CCATACATATCCCTTTGTTGGAC---CAAGACTCGTTTATTGAGCTTTCAGGGAAACACA | 1723 |
| Db | 1391 | CTCTAACAGCCCCACTCTTAGGCGATCGAGAGGACTCTGAAGTTGATTTAAATGTTCCAG | 1450 |
| Qy | 1724 | ATGTGCTCGGCTGACAGTATACGTGGCTTCTTGACACGGCCCACTCGAAACCGTGCATT | 1783 |
| Db | 1451 | ATCTTCTCACCAACCAAGTTTGAGGATGCTACTTACCGCACCAAGTCATAAAGTGCATC | 1510 |
| Qy | 1784 | ACTACTGGAGACAAATTTGATGACTCTTCATGCGACCGCTCTTTGGAGGTGCTGGCTTTG | 1843 |
| Db | 1511 | GGTACTGGGCAAGTTTGACGATGCATTCATGCGCCTATGTTTGTGTGTCGGGGATTG | 1570 |
| Qy | 1844 | TACCTTTTGTCCAGGTCTTCCAACTGA | 1871 |
| Db | 1571 | CTCTCTCGCCCTGGTCTTCCAAACGA | 1598 |

; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 38
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-607-538-38

Query Match 36.6%; Score 797.6; DB 18; Length 1620;
Best Local Similarity 69.3%; Pred. No. 8.2e-187;
Matches 1101; Conservative 0; Mismatches 484; Indels 3; Gaps 1;

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QY 287 TGTGGATCTCTAGTGTGAACTGCTTGGTATCGACATCTGATCAGCTTCTGTGG 346
DB 11 TGTGGCTTCTCTGTTTCCAAACTGGGCTCTTTGGGTACTTTCAGATCATGCTTCTGTG 70
QY 347 TTGGTTGAATCTCTTTGTTGCACTCTTTGTGCTTCTGATTTCTTTGGTCACTCTTTGG 406
DB 71 TATCATCAACCTCTTTGTGGCACTCTTTGTGCTTGCATCATCATTTGGTCACTCTTTGG 130
QY 407 AAGAAATAGATGATGAAAGAAATCCATCAACCCCTTTGTTGATTTGGGCTAGGCATGGTG 466
DB 131 AGGAAACCGCTGGTGTAAATGAGTCCATTAATGCTCCCTCATAAATGGTTGTGTACAGGAG 190
QY 467 TTACCAATTTGTTGATTAAGGAAAGCTCGCATCTTCTGCTTTTGTGTAAGATC 526
DB 191 TGGTATCTTGTCTGTAAGTGGTGAAGAAAGCACTTCTGCTTTTTCAGTGAAGATC 250
QY 527 TTTTCTTCATATATCTTTTGGCCACCAATTAATTAATGAGGCTTCAAGTAAAAAAGA 586
DB 251 TCTTTTTCATATATGTAATCTTCCCAATCATTAATGAGGCTTTCAGTAAAAAAGA 310
QY 587 AGCAATTTTTCGCAATTTTCGTAATTAATGCTTTTGTGCTGTTGTAAGTATTAATTT 646
DB 311 AGCAATTTTTCGTAATTTTCATTAATTAATGCTTTTGTGAGGCAATTTGTAAGTATTA 370
QY 647 CTTCGCAATCATATCTCTAGTGTGACACAGTTCTTTAAGAAAGTGGACATTTGGAACCT 706
DB 371 CATGTGCATTAATCATTAATGAGTGTCAATTAATTAATGAGTGTGACATTTGGAATTC 430
QY 707 TTGACTTTGGTGTATATCTTTGCTATTTGGTGCATTAATTTGCTGCAACAGATTTCAATGTA 766
DB 431 TAGATATTTGGGATTAATCTTTGCAATTTGAGCAATTAATTTGCTGCCACAGATTTCCGTCTGA 490
QY 767 CACTGCAAGTTCTGAATCAAGACGAGACACCTTTTGTCTTTTACAGTCTTTGTAATTCGGAGAG 826
DB 491 CATTCGAGTCTTACATCAGGATGAGACACCCCTCTTTTACAGTCTTTGTAATTTGGAGAAAG 550
QY 827 GTGTGTGAATGATGCAACGCTGAGTGTGCTTCAACGGATTCAGAGTTTGAATCTCA 886
DB 551 GAGTTGTAATGATGCTACATCCGCTGCTTTTCAATGCTATTAATGCTATTAATGCTTCAACCTTA 610
QY 887 CTCACCTTAAACCAAGCTGCTTTTTCATCTTCTTGAACCTTCTTGTATTTTCTCTCC 946
DB 611 CGAGGCTGAATCCAGTATAGCCCTCAGTTTCTTGGCACTTCTTCTATCTGTTCTTG 670
QY 947 TAAGTACTTGTGCTGTGCAACCGCTCTGATTAAGTGGTGAATGTTATCAAGAAGCTAT 1006
DB 671 CTAGCACTTTTACCTGGGAGCAGGAAGTGGTCTTCTTAGTGTCTTACATTAATCAAGAAGCTGT 730
QY 1007 ACTTTGGAAGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGGCTATCTTT 1066
DB 731 ATTTTGGCAGCACTCCACAGATCTGTAGGTTGCCCTTATGATGCTATGGGCTTACTTAT 790
QY 1067 CTTATATGCTTGTGAGCTTTTTCGACTTGAAGGCTATCTCTCACTGTGTTTTTCTGTGTTA 1126
DB 791 CATACATGCTGGCTGAATCTTCTATTTGAGTGGGATTTCTCACTGTATTTTCTGTGTTA 850
QY 1127 TTGTGATGTTCCCATTAATGACATGTCANATGTAACGGAGAGCTCAAGATTAACAAAGC 1186
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DB 851 TTGTAATGCTCTCATTACACTTGGCACAATGTGACCGAGATTCAGAGTCACTTACAGGC 910
QY 1187 ATACCTTTGCAACTTTGTCTATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATGG 1246
DB 911 AGCTTTTGGCAACTTTGTCTATTTCTTGGCAGAGACTTTCTCTTCTATGTCGGATGG 970
QY 1247 ATGCTTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGAAACATCGATCGCAG 1306
DB 971 ATGCTTTGGATATCGAAGAGTGGAAATTTGTTGGTGACAGGCTGGATTAATCAATTTCCG 1030
QY 1307 TGAGCTCAATTCCTAATTTGGTCTGTGTCATGTTTGGAAAGACAGCGTTCTGCTTTTCCGTTAT 1366
DB 1031 TGAGTTCAATCTGATGGAATTAATCTTCTGGGAGAGCTGCTTTGTTGTTTTCATTAAT 1090
QY 1367 CGTTTCTATTAATTTAGCCAAAGAGAAATCAAGCGAGAAATCAACTTTTAACATCGAGG 1426
DB 1091 CATTTCTTCCAACTTAATGNAAGAAATCTCTGGAGCAAAAAAATACCTTTTAGCGACAAG 1150
QY 1427 TTGTGATTTGGTGTCTGCTCATGAGAGTGTGTATCTATGCTCTTGGCTCTTGATACAACA 1486
DB 1151 TGATAATATGTTGGGAGGTTTGTATGAGAGGCGAGTGTCCATGGCACTTGGCATATAATA 1210
QY 1487 AGTTTCAAGGCGCGGCAACACAGATGTACGCGGGAATGCAATCATGATCACAGATPAGA 1546
DB 1211 AGTTCACTCTGTTGGGAGACACACTCAACTGCAGGACAAATGCAATTAATGATTAACAGCA 1270
QY 1547 TAAGTGTCTGCTTTTGTAGCAGTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1606
DB 1271 TAACCAATGTTCTATTTACGACAAATGTTATCGGTTTAAATGACAAACCCCTTATAAGTC 1330
QY 1607 ACTTATTAACGACACAGAACGCGCACACAGAGCATGTTATCTGATGACAAACCCCAAAAT 1666
DB 1331 TCTGCTGCCACCAACAGAGGCAATTTGAGTACAGTGTCTACAGTGCATAATCTCCAAAGT 1390
QY 1667 COATACATATCCCTTTTGTGGAC---CAAGACTGTTTCAATGAGCTTTCAGGGAACCA 1723
DB 1391 CTCCTAACGCCCCACTCTCTAGGAGTTCGAGAGGACTCTGAAAGTTGATTTAAATGTTCCAG 1450
QY 1724 ATGTGCTCTGGCTGACAGTATACGTGCTTCTTGCACGCGCCACTCGAACCGTGCATT 1783
DB 1451 ATCTTCTCTCACCAACCAAGTTTGGAGTGTACTTACCGCACCAAGTATAAAGTGCATC 1510
QY 1784 ACTACTGGAGACAAATTTGATGATCTCTTTCATCGACCCGCTCTTTGGAGTCTGTTGGTTG 1843
DB 1511 GGTACTGGCGCAAGTTTTCAGGATGCAATTCATGCGCCCTATGTTTGGTGGTGGGATTTG 1570
QY 1844 TACCCTTTGTTCCAGGTTCTTCCAACTGA 1871
DB 1571 CTCCTCTGCCCCCTGGTTCTCCAAACGGA 1598
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RESULT 10

US-10-369-324-37
; Sequence 37, Application US/10369324
; Publication No. US20030221213A1
; GENERAL INFORMATION:
; APPLICANT: ROMMENS, CAIUS
; APPLICANT: YE, JINGSONG
; APPLICANT: MENENDEZ-HUMARA, JAIME
; APPLICANT: YAN, HUA
; APPLICANT: RICHARD, CRAIG
; APPLICANT: BRINKERHOFF, W. LEIGH
; APPLICANT: SWORDS, KATHY M. M.
; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0162
; CURRENT APPLICATION NUMBER: US/10/369,324
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 124

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-369-324-37

Query Match      36.5%; Score 794.4; DB 17; Length 1621;
Best Local Similarity 69.2%; Pred. No. 5.1e-186;
Matches 1099; Conservative 0; Mismatches 486; Indels 3; Gaps 1;

QY 287 TGTGATCTCTAGTGTGAACTGCTTCTGTTATCGACATCTGATCAGCTTCTGTGG 346
Db 11 TGTGCTCTCTCTGTTTCCAAAACCTGGCTCTTTGGGTACTTCAGATCATGCTCTGTG 70
QY 347 TTGCGTTGAATCTCTTTTGTGCACTTCTTTGTGCTTGTATTTGTTCTTGTGTCATCTTTTGG 406
Db 71 TATCCATCAACCTCTTTTGTGGCACTCTTTGTGCTTGTGATCATCAITTTGGTCACTCTCTGG 130
QY 407 AGAGAAATAGATGATGAAGAAATCAATCAACCCCTTGTGATTTGGGCTAGGCACTGGTG 466
Db 131 AGAGAAACCGCTGGGTAAATAGATGATCACTTACTGCCCTCAATTTGGTGTGTGTACAGGAG 190
QY 467 TTACCAATTTTGTGATTTAGTAAAGGAAAGCTCGCATCTTCTGCTTTTAGTGAAGATC 526
Db 191 TGGTTATCTTGTCTCGTAAGTGTGGAAGAGCTCACACCTTCTGCTTTTCAAGTGAAGATC 250
QY 527 TTTTCTTCATATATCTTTTGCCACCCATATATTTCAATGAGGCTTTCAAGTAAAAAAGA 586
Db 251 TCTTTTTCATATATGATCTCTCTCCATCATATTTAATGAGGCTTTTCAAGTAAAAAAGA 310
QY 587 AGCAGTTTTCGCAATTTGCGTACTATATAGCTTTTGTGCTTTTGTGCTTTTGTGCACTATTATT 646
Db 311 AGCAATTTTTCGTAACCTTCATTAATGATGATTTGAGGCAATTTGATACCTCTGCTCT 370
QY 647 CTGTCACATCATCTCTAGTGTAAACAGTCTTTTAAAGTGTGGAATTTGGAACCT 706
Db 371 CATGTGCCATATATCATTAAGTGTGCAATTTCAAACTTTCAAGAGTTGGAATTTTC 430
QY 707 TTGACTTGGTGTATATCTTGTATTTTGTGCTTATTTGCTCAACAGATTTCAAGTATGTA 766
Db 431 TAGTATTTGGGATTTATCTGCAATTTGGAGCATATTTGCTGCCACAGATTCGCTCTGCA 490
QY 767 CACTGAGGTTCTGAATCAAGACGAGACACCTTTTGTGCTTTTACAGCTTTGATTCGGAGAG 826
Db 491 CATTCAGGTCCTACATCAGATGAGACACCCCTCTTTACAGCTTTGATTTGGAGAG 550
QY 827 GTGTTGTGATGATGCAACGTCAGTTGTGCTTTCAACGGATTCAGAGCTTTGATCTCA 886
Db 551 GAGTTGTAATGATGTACATCGTGTGCTTTTCAATGCTATTTCAAACTTCGACCTTA 610
QY 887 CTCACCTAAACACGAGCTGCTTTTTCATCTCTTGGAACTTTCTTGTATTTTCTCTCC 946
Db 611 CGAGCATGAATCCAGATAGCCCTCAGTTTCTTGGCACTTCTCTATCTGTTCTCTTG 670
QY 947 TAAGTACCTTGTGCTGTGCAACCGCTCTGATAAGTGGTATGTTATCAAGAAGCTAT 1006
Db 671 CTAGCACTTTACTGGGAGGAGAACTGCTCTTCTTAGTCTTACATTAATCAAGAAGCTAT 730
QY 1007 ACTTTGGAAGGCACTCACTGACCGAGAGTTGCCCTTATGATGCTTATGGCGATCTTT 1066
Db 731 ATTTTGGCAGGCACTCCACAGATCGTGAGGTTGCCCTTATGATGCTCATGCTTACTTAT 790
QY 1067 CTTATATGCTGTGAGCTTTTCGACTTGAGCGGTATCTCTCACTGTGTTTTTCTGTGGA 1126
Db 791 CATACTTGTGCGCGAATTAATCTATTGAGTGGGATTTCTACCGCTTTTCTGTGGTA 850
QY 1127 TTGTGATGTCCTTACATGATGCAATGTTAAACGGAGAGCTCAAGAAATAACAAGAAGC 1186
Db 851 TTGTATGCTCACTACACTTGGCACAATGTGACCGAGGATTCAGAGTCACTACAAGGC 910
QY 1187 ATACCTTTGCACTTTGTGCAATTTCTTGGGAGACATTTATTTTCTGTATGTTGGAATGG 1246
Db 1187 ATACCTTTGCACTTTGTGCAATTTCTTGGGAGACATTTATTTTCTGTATGTTGGAATGG 1246
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RESULT 11

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US-10-607-538-37
; Sequence 37, Application US/10607538
; Publication No. US20040107455A1
; GENERAL INFORMATION:
; APPLICANT: ROMMENS, CATUS
; APPLICANT: YE, JINGSONG
; APPLICANT: HUMARA, JAIME M.
; APPLICANT: YAN, HUA
; APPLICANT: SWORDS, KATHY
; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0167
; CURRENT APPLICATION NUMBER: US/10/607,538
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 10/369,324
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Solanum tuberosum
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QY 446 TGAATGGCTAGGCACTGGTGTACCAATTTTGTGATTAGTAAAGAAAAGCTCGCATC 505
DB |||||
QY 170 TCAATGGTTCGTGTACTGGGATGTGATCTTGTCTTAAGTGGAGGCAAAAGCTCAAGGA 229
DB |||||
QY 506 TTCTCGCTTTAGTGAAGATCTTTTCTTCATATATCTTTTGGCCACCCCAATTATATCAATG 565
DB |||||
QY 230 TTCTTGTGTAGTGAAGATCTCTCTTTATTTATCTTCTCCACCAATTATATCAACG 289
DB |||||
QY 566 CAGGTTTTCAAGTAAAGAAAGAGAGTTTTTCCGCAATTTTGGTCACTATATATGCTTTTG 625
DB |||||
QY 290 CAGGTTTTCAAGTAAAGAAAGAGCAATTTTTCGCAATTTTCAATGACCAATTATGTTATTG 349
DB |||||
QY 626 GTGCTTTGGGACTATTATTTCTTGCACAATCATATCTCTAGGTGTAAACACAGTTCTTTA 685
DB |||||
QY 350 GTGCTTTGGAACTCTCATTTTCAATTTGTATCATCTCATTTGGTGTAAACATCTTTTCG 409
DB |||||
QY 686 AGAAGTTGGACATTTGGAACTTTGACTTGGGTGATATCTTGTCTTATTTGGTGCCTATTTG 745
DB |||||
QY 410 AGAAAATGAATATCGGTGATCTTACCAATTCGGACTATCTAGCCATTTGGAGCAATATCT 469
DB |||||
QY 746 CTGCAACAGATTCAGTATGATACCTGAGGTTCTGAATCAAGACGAGACACCTTTGCTTT 805
DB |||||
QY 470 CTGCTACAGACTCTGTTTGCACCTTGTCAAGTGTAAATCAAGACGAGACACCTCTCTGT 529
DB |||||
QY 806 ACAGTCTTTGATTCGGAGAGGCTGTGTGAATGATGCAAGCTCAGTTGTGCTCTTCAACG 865
DB |||||
QY 530 ACAGTCTTTGTTGGAGAGGTTGTGTGAAGATGCAATCTCGTCTGCTCTTCAATG 589
DB |||||
QY 866 CGATTCAGAGCTTTGATCTCACTCACCTAAACCAAGCTGCTTTTCACTCTTTGGAA 925
DB |||||
QY 590 CAATACAGAGATTCGACCTCACAAATATCAATTCAGCCATAGCTTTGGAGTTTGGTGGAA 649
DB |||||
QY 926 ACTCTTGTATTTGTTCTCTAAGTACTTGTCTGTGCTGCAACCGGTCTGATAGTG 985
DB |||||
QY 650 ACTTTTTCCTTTTATCTTAAGACAGACTTGTGTGAGCTGGATTCCTCAGTG 709
DB |||||
QY 986 CGTATGTTATCAAGAGCTATCTTTGGAAGGCACTCACTGACCCAGAGGTTGCCCTTA 1045
DB |||||
QY 710 CTTTGTGTTATCAAGAGCTCTATATAGGAAGGCACTCTACTGATCGTGAATGGCACTTA 769
DB |||||
QY 1046 TGATGCTTATGGGTATCTTTCTATATGCTTGTGCTGAGCTTTTCGACTGAGCGGTATCC 1105
DB |||||
QY 770 TGATGCTTATGGCTTACTTATCATATATGTTGACAGAGCTATTCACCTTGAGCTCTATCT 829
DB |||||
QY 1106 TCACTGTGTTTCTGTGGTATTTGTGATGTGCCATACATGCGCAATGTAAACGGAGA 1165
DB |||||
QY 830 TGACTGTGTTCTTCGGGATTTGTATGTCTCACTATACATGCGCAATGTACAGATA 889
DB |||||
QY 1166 GCTCAAGAAATAACAACAGCATACCTTTGCAACTTTGTCAATTTCTGCGGAGACATTTA 1225
DB |||||
QY 890 AATCCAAGGTCACTACAAAACATACTTTTGTGCAATGTCTTCTAGCTGAGATTTTGA 949
DB |||||
QY 1226 TTTTCTGTATGTTGGAATGGATCCCTTGGACATTCAGAGTGGAGATCGTGAAGTACA 1285
DB |||||
QY 950 TCTTCTTACGTTGGAATGGACGCTCTGATATCGAGAAATGGGACGTTGTACGCAACA 1009
DB |||||
QY 1286 CACCGGAAACATCGATCGAGTCACTCAATCTTAATGGTCTGCTGATGTTGGAAGAG 1345
DB |||||
QY 1010 GTCTGTGTCAGTTCGATTTGAGTTAGTTCAATCTTCTGGCTTATCTTCTGGGTGCGG 1069
DB |||||
QY 1346 CAGGTTTGTCTTTCGGTTATCGTTTCTATCTAATCTAGCCAAAGAAATCAAAAGCGAGA 1405
DB |||||
QY 1070 CCGCGTTTCGTTTTCACCTTCTTCTGTCCAATTTAAACAAAGTCTTCAACCGGATGAGA 1129
DB |||||
QY 1406 AAATCAACTTTTAAATGAGTTGTGATTTGTGTTGCTGCTCATGAGAGGCTGTGAT 1465
DB |||||
QY 1130 AAATAGACTTAAAGAAACAAAGTAACCAATTTGGTGGGCTGGTCTGATGCGGTGGTGTG 1189
DB |||||
QY 1466 CTATGGCTCTTGATACAACAGTTTAAAGGGCCGGGACACAGATGTACCGGGAATG 1525
DB |||||
QY 1190 CAATGGCTCTTGTTATTAACCAAGTTTCAACAACTTCAGGACACACCAAGGTTCTTGGGAAG 1249
DB |||||

QY 1526 CAATCATGATCAGAGTACGATAAATCTGTCTGCTTTTATAGCACAGTGTGTTGGTATGC 1585
DB |||||
QY 1250 CTATCATGATCAGAGTACCATCAGTGTGTTCTTTTTCAGTACTGTGGTGTGTTGGATTC 1309
DB |||||
QY 1586 TGACCAAAACCACTCATAAAGCTACTATTACCGCACACAGAACGCCACACAGAGCATGTTAT 1645
DB |||||
QY 1310 TAACCAAAACCGTTAGTCAAAACATTTTCAGCCCTTCATCAAAACAGTCTCTCCACGACCGCG 1369
DB |||||
QY 1646 CTGATGACAAACACCCCAAAATCATACATATCCCTTTTGTGGACCAAGACTCGTTCAATG 1705
DB |||||
QY 1370 TGCAGATCACACTAAGATCTTCTTTCACGATCCGATCTCCATGAGCCGTTGCTCAGTA 1429
DB |||||
QY 1706 AGCTTTCCAGGAACCAACATGTCCT---CGSCCTGACAGTATAGTGGCTTCTTGACAC 1762
DB |||||
QY 1430 CCGAAGCCAGTCAAGATACGACCTTGAACAAATGTTAGCTTCAAGATGTTCTGGAAT 1489
DB |||||
QY 1763 GGCCCACTCGAACCCGTGCAATTACTACTGGAGACAAATTTGATGACTCTTTCATGCGACCGG 1822
DB |||||
QY 1490 CTCGCTCCAGGGCCATTCATCATTACTGGAGAAATTCGATAACGAGTTATGCGTCGCA 1549
DB |||||
QY 1823 TCTTTGGAGGTCGTGGCTTTGTACCTTTTCCAGGTTTCCAACTGAGAGAAACCCCTC 1882
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QY 1550 TATTTGGTGGCCGAGGCGTTTCCACAGTAGTTCCAGGTTCACCCATTGAGAATAGTGTTC 1609
DB |||||
QY 1883 CTGATCTTAGTAAGCTTTCAGGGTAACTGGAAGAAAAG 1921
DB |||||
QY 1610 CCGAATGGAGTGAAGAGTAGAAGAAACAAAGAACG 1648
DB |||||

RESULT 14

US-10-409-701-22
; Sequence 22, Application US/10409701
; Publication No. US20030221224A1
; GENERAL INFORMATION:
; APPLICANT: Zinselmeier, Chris
; APPLICANT: Helentjaris, Timothy G.
; FILE OF INVENTION: Enhanced Silk Exsersion Under Stress
; FILE REFERENCE: 1421
; CURRENT APPLICATION NUMBER: US/10/409,701
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,796
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1638)
US-10-409-701-22

Query Match 31.3%; Score 682.6; DB 17; Length 1638;
Best Local Similarity 65.6%; Pred. No. 2.7e-158;
Matches 1029; Conservative 0; Mismatches 534; Indels 6; Gaps 2;

QY 318 GTTATCGACATCTGATCAGCTTCTGTGGTTGCGTTGGAATCTCTTTGTTGCACTTCTTTG 377
DB GCTCTCGGTCTCGGATCAGGACCGCATCGTCTCGAATTAACATCTTCATCGCGGCTGCTCG 98
QY 378 TGCCTTGTATTGTTCTTGGTCACTCTTTTGGAAAGAGAATAGATGGATGAACGAATCCATCAC 437
DB 99 CAGCTGCATCTGATCGGCCACTTGTCTGGAAGGNAACGATGGGTGAACGAGTCCATCAC 158
QY 438 GCGCTTGTGATTGGGTAGGCACTGGTGTACCATTTTGTGTTAGTAAAGAAAG 497
DB 159 GCGCTTGTGATGGGCTTCATCAGCGAGGCGTCATCTGCTGTTTACTATATGGGACAAA 218
QY 498 CTCGATCTCTCTGCTTTAGTGAAGATCTTTTCTCATATATCTTTTCCACCCCATTTAT 557
DB 219 CTCAGGCATCTTGTGTTACGAGGACCTGTTTTCATATATTTACTTCCGCCGATAT 278

QY 558 ATTCAATGCGAGGTTTCAAGTAAAAAAGAGCAGTATTTTCCGCAATTTCTGTGACTATTAT 617
DB 279 CTTCAATGCGGGTTTCAAGTAAAGAAAAGCAATTTCTTCGCAACTTTATAACGATTAT 338
QY 618 GCTTTTGGTGTGTTGGGACTATTATTTCTGCACAAATCATATCTCTAGGTGTAAACACA 677
DB 339 TTTGTTTGGTGTATTGGGACTGTGATTTCTTTGTAATATCTCTCTGGTGTCTATGGG 398
QY 678 GTTCTTTAAGAAAGTTGGACATTTGGAACCTTTGACTTTGGGTGATTTATCTTGTCTATTGGTGC 737
DB 399 GTTGTTCACAGAACTTGTGTTGGTCCACTCGAGCTTGGGGACTATCTTTGCAATTTGGTGC 458
QY 738 CATATTTGCTGCAACAGATTCAGTATGTACACTGCGAGTTCTGAATCAAGACAGACACC 797
DB 459 TATTTTCTCGGCAACAGATTTCTGTTTGCACCTTACAGGTGCTTTAACCAGGATGAAACACC 518
QY 798 TTTGCTTTACAGTCTTGTATTGCGAGAGGGTGTGTAATGATGCAAGCTGAGTTGGT 857
DB 519 CCTACTCTATAGTCTAGTTTGGTGAAGGTGTGTTAATGATGCCACATCTGTGTTGCT 578
QY 858 CTTCAACGCGATTCAGAGCTTTGATCTCACTCACTTAAACCAAGCAAGCTGCTTTTCATCT 917
DB 579 CTTCAATGCAATTTGAAACCTTGATATGATAATTTTGATGCTATTGTTCTGTGTAATTT 638
QY 918 TCTTGGAAACTTCTGTATTTGTTTCTCTTAAGTACTTGTCTGGTGTGCTGCAACCGGTCT 977
DB 639 CGTCGGAAAAATTTCTACTTGTCTTCCACGACCATACTTTGGAGTAGCTACACGGGTT 698
QY 978 GATAAGTGGGTATGTTATCAAGAAAGCTATACTTTGGAAGCACTCAACTGACCGAGAGGT 1037
DB 699 GCTTAGTGACATCAATTTATCAAGAGCTCTGTTTGGCAGACATTTCACTGTATGAGAAGT 758
QY 1038 TGCCTTTATGATCTTATGCGGTATCTTCTTATATGCTTGTGAGCTTTTCGACTTTGAG 1097
DB 759 TTTCTATCATGACTACTCATGSCATACCTTTTATCATATGATATCAATGCTGTGTGACCTGAG 818
QY 1098 CGGTATCTCAGTGTGTTTCTGTGATTTGTGATGTGATGCTCCATTAACATGGCAATGT 1157
DB 819 TGGAAATCTTACTGTCTTCTCTGTGGAATGATGATGTCACATTTACATTTGGCATATGT 878
QY 1158 AACGGAGAGCTCAAGATAACAAAGCATACCTTTGCAACTTTGTCATTTCTTCGGA 1217
DB 879 GACAGAAAGTTCTAGGGTTACCAAGCAGCATCTTTTGCACATTTATCATTTCAATTCGAGA 938
QY 1218 GACATTTATTTCTTGTATGTTTGGAAATGATGCTTGTGACATTTGCAAGTGGAGATCCGT 1277
DB 939 AATTTTCTCTCTCTATGTTGGATGATGATGATTTGGACATTTGAGAGTGGAAATAGC 998
QY 1278 GAGTGACACACCGGGAACTCGATCGAGTGAAGTCAATCTTAATGGGTCTGTCTATGGT 1337
DB 999 TAGTAGCAGTCTTAAGAAACCAATTCGTTTAAAGTGCAATTTATTTTGGGCTTGGTTATGGT 1058
QY 1338 TGAAGAGCAGCGTTCGTTCTTCGTTATGCTTTCTATCTTAAGTACCAAGAGATCA 1397
DB 1059 TGAAGAGCGGCATTTGTATCCCTTTGCTGTTCTTATCCACTTAAGCAAAAGAGGC 1118
QY 1398 AAGCGAGAAAAATCAACTTTAAACATGAGGTGTGATTTGGTGTCTGTTCTCATGAGAGG 1457
DB 1119 CCGTCCAAAGATCTCTTCAAGCAACAGTAATCATATGTTGGGTGTTCTCATGAGAGG 1178
QY 1458 TGTGTATCTATGGCTCTTGATACAAAGTTTAAAGGGCGGGGCAACAGATGTACG 1517
DB 1179 AGCAGTGTCAATTGGCTTGGCTTATAAAGTTTACAGCATCTGTTCAACTGAAGTGGC 1238
QY 1518 CGGGAATGCATCATGATCAGGATGAGTAACTGCTGCTTTTATGACAGTGTGTT 1577
DB 1239 AGTCAATGCTATCATGATCACCAGCAGTATTTGTTGTTTCTTATTCAGCACAATGTTTT 1298
QY 1578 TGTATGCTGACCAAAACCTCATAGTACCTTATTAACCGCACCAAGCGCCACACGAG 1637
DB 1299 CGGCTGCTGACGAGCGGTGCTGATCTCTCTCATCCAC-CAAGACTGGACTGAACA 1357
QY 1638 CATGTTATCTGATGACAAACCCCAAAATCCATATATATCCCTTTTGTGGACCAAGACTC 1697

DB 1358 CGTGTCTCTGCTCTCAAGCCAGTCTATGCTGAGCCACCTCTTACTAGCATGA-----T 1412
QY 1698 GTTCATTGAGCCTTCAGGGAAACCAAAATGTGCTCGGCTCGACAGTATACGTGGCTTCTT 1757
DB 1413 GGGGTCTGACTTTGATGTAGGCGAGATCAATCCCTCAATACAACTCCAGTTCATTCT 1472
QY 1758 GACACGGCCACTCGAACCGTGCATTTACTATGAGACAAATTTGATGACTCTCTTCATGCG 1817
DB 1473 CACCGCGCAGCTCGCTCGTCCATCGCTTTTGGCGCAAGTTTGGACGATCGGTTCAATGG 1532
QY 1818 ACCGCTTTTGGAGTCTGCTGCTTTGTAACCTTTGTTCCAGGTTCTCCAACTCAGAGAAA 1877
DB 1533 CCGGTGTTTGGGGGGCGAGGTTTCTCCCTTTTGTGCTTGGTTCGCGGTGAGAGGAG 1592
QY 1878 CCTCCTGA 1886
DB 1593 TGTCCCTGA 1601

RESULT 15
US-10-425-115-153633
; Sequence 153633, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 153633
; LENGTH: 2222
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_71692C.1
US-10-425-115-153633

Query Match 31.3%; Score 682.6; DB 18; Length 2222;
Best Local Similarity 65.6%; Pred. No. 3.1e-158;
Matches 1029; Conservative 0; Mismatches 534; Indels 6; Gaps 2;

QY 318 GTTATCGACATCTGATCAGCTTCTGTGGTTCGTTGGAATCTCTTTGTTGCACTTCTTTG 377
DB 263 GCTCTGGTCTCGGATCAGCGCCATCTGCTCGATTAAACATCTTCATCGCTGCTCTG 322
QY 378 TGTCTGATTTGTTCTTGGTTCATCTTTTGAAGAGATAGATGGAAGAAATCCATCAC 437
DB 323 CAGCTGCATTTGTCATCGGCACTTGTCTGAGGGAACCGATGGGTGAAACGAGTCCATCAC 382
QY 438 CGCTTTGTTGATGGGCTAGGCACCTGTGTACCAATTTTGTGATTAAGAGAAAG 497
DB 383 CGCGCTTGTATGGGCTCATCACGAGGCGTTCATCTGCTGTTTACTTAATGGGACAA 442
QY 498 CTCGCATCTTCTGCTTTTGTGAGATCTTTTCTCATATATCTTTTGCACCCATTAT 557
DB 443 CTCACGATTTTGTGTTTCAGCGAGACCTGTTTTCATATATTTTACTTCCCGCCGTAAT 502
QY 558 ATTCAATGAGGTTTCAAGTAAAAAAGACAGATTTTCCGCAATTTCTGTGACTATTAT 617
DB 503 CTTCAATGCGGGTTTCAAGTAAAGAAAGCAATTTCTTCGCAACTTTATAACGATTAT 562
QY 618 GCTTTTGGTGTGTTGGGACTATTATTTCTTGCACAAATCATATCTCTAGGTGTAAACA 677
DB 563 TTTGTTGGTGTATTGGGACTCTGATTTCTTTGTAATAATCTCTCTCTGTTGCTATGGG 622
QY 678 GTTCTTTAAGAGTTGGACATTTGGAAACCTTTGACTTGGGTGATTTATCTTGTCTATTGGTGC 737

Db 623 GTTGTTCAGAAACTTGATGTGGTCCACTCGAGCTTGGGGACTATCTTGCATTTGGTGC 682
Qy 738 CATATTTGCTGCAACAGATTTCAGTATGTATACACTCGAGGTTCTGAATCAAGACGAGACACC 797
Db 683 TATTTTCTCGSCAACAGATTCTGTTTGACCTTACAGGTGCTTAAACGAGATGAAACACC 742
Qy 798 TTTCGCTTACAGTCTTGTATTTGGAGAGGGTGTGTGAATGATGCAACGTCAGTTGGT 857
Db 743 CCTACTCTATAGTCTAGTTTGGTGAAGGTGTGTGAATGATGCAACGTCAGTTGGT 802
Qy 858 CTTCAACGCGATTTCAGAGCTTTGATCTCACTCACTTAACCAACGAACTGCTTTTCATCT 917
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Qy 918 TCTTGGAAACTTCCTGATTTGTTTCTCTTAAGTACCTTGTGGTGTGCTCAACCGGTCT 977
Db 863 CGTCGAAATTTCTCTACTTGTCTTACCAGCACCATCTTGGAGTAGCTACCGGTT 922
Qy 978 GATAGTCCGTATGTTATCAAGAGCTATACCTTTGGAAGGCACTCAACTGACCGAGAGGT 1037
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Qy 1038 TGCCCTTATGATGCTTATGGGTATCTTCTTATATGCTTGTGAGCTTTTCGACTTTGAG 1097
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Db 1043 TGGAAATTCCTACTGCTCTCTCTGTGGAATAGTAATGTACATTAACATTTGGCATAATGT 1102
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Db 1103 GACAGAAAGTTCTAGGGTTTACCAACAGCATCTTTTGGCAACTTTATCATTTCAATTGCGA 1162
Qy 1218 GACATTTATTTCTTGTATGTTGGAATGGATGCTTGGACATTTGACAAAGTGGAGATCCGT 1277
Db 1163 AATTTTCTCTTCTCTATGTTGGATGATGATTTGGACATTTGAGAGTGGAAATTAGC 1222
Qy 1278 GAGTGACACACCGGGAACATCGATTCGAGTCAATCCTAATGGTCTGCTCATGTT 1337
Db 1223 TAGTAGCAGTCTTAAGAAACCAATTTGCTTTAAGTGCAATTTATTTGGGCTTGGTTATGTT 1282
Qy 1338 TGGAGAGCAGCTTCTGCTTTCCGTTATCGTTTCTATCTAATCTAGCCAGCAAGAAATCA 1397
Db 1283 TGGAGAGCGGCAATTTGTATTCCTTTGTGCTTCTTATCCACCTAAGCAAAAGGAGGC 1342
Qy 1398 AAGCAGAAATCAACTTTAAATCATGAGGTGTGATTTGGTGTGCTGCTCATGAGAGG 1457
Db 1343 CCGTCCAAAGATCTCCTTCAAGCAACAGTAATCATATGTTGGGCTGGTCTCATGAGAGG 1402
Qy 1458 TGCTGTATCTATGGCTCTTGCAATACAAAGTTTAAAGGGCGGGCAACAGATGTACG 1517
Db 1403 AGCAGTGTCAATTTGCGCTTATACAGATTTACAGATCTGCTCACTGAAGTGGC 1462
Qy 1518 CGGGAATGCAATCATGATCAGAGTACGATACGTTCTGCTTTTGTAGCAGTGGTGT 1577
Db 1463 AGTCAATGCTATCATGATCACCAGCAGTTATTTGTTTCTTATTCAGCACATGGTTTT 1522
Qy 1578 TGATATGCTGACCAACCACTCATAGCTACCTATTACCGCACCAAGACCGCCACACGAG 1637
Db 1523 CGGCTGTGACGAAGCGCTGCTAGTCTCTCTCATCCAC - CAAGGACTGGACTGAACA 1581
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Db 1582 CGTCGTCTCTGCTCTCAAGCAGTCTATGCTGGACCCACTCTCTTACTAGCATGA - - - - -T 1636
Qy 1698 GTTCATTTAGCCCTTCAGGGAACCAATGTGCTCGGCTGACAGTATACGTGGCTTCTT 1757
Db 1637 GGGGCTGACTTTGATGTAGGGGAGATCACTCCCTCAATCAACTCAAGTTCAITCT 1696
Qy 1758 GACACGGCCCACTCGAACCGTGCATTTACTATGGAGACAATTTGATGACTCCTTCATGCG 1817
Db 1697 CACCGGCGCAGCTCGCTCCGCTCCATCGCTTTGGCGCAAGTTTGAAGTCGGTTTCATGCG 1756

Qy 1818 ACCCGTCTTTGGAGGTCTGGCTTTTGTACCCCTTTGTTCCAGGTTCTCCAACTGAGAGAA 1877
Db 1757 CCGGTGTTCCGGGGCGGAGGTTTCGTCCCTTTGTTGCTTGGTTCGCGGTGAGAGGAG 1816
Qy 1878 CCCTCCTGA 1886
Db 1817 TGTCCCTGA 1825

Search completed: April 26, 2005, 09:32:06
Job time : 2810 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 03:34:19 ; Search time 384 Seconds
(without alignments)
9280.757 Million cell updates/sec

Title: US-10-617-623-1
Perfect score: 2178
Sequence: 1 cctctctgttctgtctctcg.....aaaaaaaaaaaaaaaaaaaaa 2178

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|---------|---------------------|---------------------|
| 1 | 821.2 | 37.7 | 2553 | US-09-830-123-16 | Sequence 16, Appl |
| 2 | 813 | 37.3 | 2423 | US-09-830-123-14 | Sequence 14, Appl |
| 3 | 774.8 | 35.6 | 2237 | US-09-830-123-1 | Sequence 1, Appl |
| 4 | 754.4 | 34.6 | 2361 | US-09-830-123-18 | Sequence 18, Appl |
| 5 | 91.2 | 4.2 | 1581 | US-09-800-729-22 | Sequence 22, Appl |
| 6 | 64.4 | 3.0 | 1354 | US-09-800-729-58 | Sequence 58, Appl |
| 7 | 64.4 | 3.0 | 1688 | US-09-800-729-57 | Sequence 57, Appl |
| 8 | 60.6 | 2.8 | 4452 | US-09-949-016-849 | Sequence 849, Appl |
| 9 | 59.8 | 2.7 | 4460 | US-09-949-016-4129 | Sequence 4129, Appl |
| 10 | 53.8 | 2.5 | 1291 | US-09-524-101D-5 | Sequence 5, Appl |
| 11 | 53.8 | 2.5 | 2007 | US-08-747-221B-36 | Sequence 36, Appl |
| 12 | 53.8 | 2.5 | 2007 | US-08-747-221B-38 | Sequence 38, Appl |
| 13 | 53.8 | 2.5 | 2007 | US-09-005-051-36 | Sequence 36, Appl |
| 14 | 53.8 | 2.5 | 2007 | US-09-005-051-38 | Sequence 38, Appl |
| 15 | 53.8 | 2.5 | 2007 | US-09-403-942F-36 | Sequence 36, Appl |
| 16 | 53.8 | 2.5 | 2007 | US-09-403-942F-38 | Sequence 38, Appl |
| 17 | 53.6 | 2.5 | 17612 | US-09-949-016-15061 | Sequence 15061, A |
| 18 | 50 | 2.3 | 1141 | US-09-806-708B-22 | Sequence 22, Appl |
| 19 | 48.8 | 2.2 | 1169 | US-09-100-391-5 | Sequence 5, Appl |
| 20 | 48.8 | 2.2 | 1169 | US-09-616-614-5 | Sequence 5, Appl |
| 21 | 48.8 | 2.2 | 1302 | US-09-100-391-11 | Sequence 11, Appl |
| 22 | 48.8 | 2.2 | 1302 | US-09-616-614-11 | Sequence 11, Appl |
| 23 | 48.8 | 2.2 | 2643 | US-09-100-391-9 | Sequence 9, Appl |
| 24 | 48.8 | 2.2 | 2643 | US-09-616-614-9 | Sequence 9, Appl |
| 25 | 48.4 | 2.2 | 684 | US-09-248-796A-6653 | Sequence 6653, Appl |
| 26 | 48.4 | 2.2 | 1664976 | US-08-916-421B-1 | Sequence 1, Appl |
| 27 | 48.4 | 2.2 | 1664976 | US-09-692-570-1 | Sequence 1, Appl |

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|----|------|-----|--------|---|---------------------|-------------------|
| 28 | 47.8 | 2.2 | 832 | 4 | US-09-621-976-2813 | Sequence 2813, Ap |
| 29 | 47.6 | 2.2 | 915 | 4 | US-09-601-198-7 | Sequence 7, Appl |
| 30 | 46.6 | 2.1 | 5852 | 1 | US-07-867-106-2 | Sequence 2, Appl |
| 31 | 46.4 | 2.1 | 640681 | 4 | US-09-790-988-1 | Sequence 1, Appl |
| 32 | 46 | 2.1 | 505 | 4 | US-09-621-976-15639 | Sequence 15639, A |
| 33 | 46 | 2.1 | 3138 | 1 | US-07-867-106-4 | Sequence 4, Appl |
| 34 | 45.4 | 2.1 | 1466 | 3 | US-08-984-919A-10 | Sequence 10, Appl |
| 35 | 45.4 | 2.1 | 1466 | 3 | US-08-984-919A-12 | Sequence 12, Appl |
| 36 | 45.4 | 2.1 | 1472 | 3 | US-08-781-420-10 | Sequence 10, Appl |
| 37 | 45.4 | 2.1 | 1472 | 3 | US-08-781-420-12 | Sequence 12, Appl |
| 38 | 45.4 | 2.1 | 1472 | 3 | US-08-874-102-10 | Sequence 10, Appl |
| 39 | 45.4 | 2.1 | 1472 | 3 | US-08-874-102-12 | Sequence 12, Appl |
| 40 | 45.4 | 2.1 | 1472 | 3 | US-09-006-595A-10 | Sequence 10, Appl |
| 41 | 45.4 | 2.1 | 1472 | 3 | US-09-006-595A-12 | Sequence 12, Appl |
| 42 | 45.4 | 2.1 | 1875 | 3 | US-08-984-919A-46 | Sequence 46, Appl |
| 43 | 45.4 | 2.1 | 1875 | 3 | US-08-984-919A-48 | Sequence 48, Appl |
| 44 | 45.4 | 2.1 | 1881 | 3 | US-08-874-102-46 | Sequence 46, Appl |
| 45 | 45.4 | 2.1 | 1881 | 3 | US-08-874-102-48 | Sequence 48, Appl |

ALIGNMENTS

RESULT 1
US-09-830-123-16
; Sequence 16, Application US/09830123
; Patent No. 6803500
; GENERAL INFORMATION:
; APPLICANT: Iida, Shigeru
; APPLICANT: Tanaka, Sachiko
; APPLICANT: Inagaki, Yoshihide
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles
; FILE REFERENCE: 001560-397
; CURRENT APPLICATION NUMBER: US/09/830,123
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/JP00/05722
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: JP 11/236800
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 2553
; TYPE: DNA
; ORGANISM: Nierebergia hybrida
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(2553)
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the pH of vacuoles
; OTHER INFORMATION: pH of vacuoles
US-09-830-123-16

| | | | | |
|-----------------------|-----------------|---|-----------|--------------|
| Query Match | 37.7%; | Score 821.2; | DB 4; | Length 2553; |
| Best Local Similarity | 70.3%; | Pred. No. 28-199; | | |
| Matches 1115; | Conservative 0; | Mismatches 468; | Indels 3; | Gaps 1; |
| QY | 289 | TTGGATTCTCTAGTGTGCAAACTGCTTTCGTTATCGACATCTGATCAGCTTCTCTGTGGTT | 348 | |
| DB | 543 | TTTGGGACTCTGCTGGGAAGATGAACAACCTTCTGATCATCAATCAGTGGTG | 602 | |
| QY | 349 | GGTTGAATCTCTTTGTGGCACTCTTTGTGCTGTATTTGTTGCTGATCTTTTGGAA | 408 | |
| DB | 603 | TCGGTAAACTTTTGTGCACTTATTTGCGGCTGTATTTGATCGTCAITTTATTGGAG | 662 | |
| QY | 409 | GAGATAGATGATCAACGATCCATCCCGCTTGTGATTTGGCTAGGCTAGCTGTGTT | 468 | |
| DB | 663 | GAACACAGATGATGAATGAGTCCATACTGCCCTTGTGATTTGGTATTTGCTGAGTCT | 722 | |
| QY | 469 | ACCATTTTGTGATTTAGTAAAGAAAAAGCTCGCATCTTCTGCTCTTTAGTGAAGATCTT | 528 | |
| DB | 723 | ATCATTTCTACTAATTAAGTGGAGGAAGAACTACATATTTTAGTGTTCAGCGAGATCTT | 782 | |
| QY | 529 | TTCTTCATATATCTTTTTCGCCACCCATATATTAATCAATGACGGGTTTCAAGTAAAAAAGAG | 588 | |

Db 693 GCTCTTTGGGGCACTTGGGACCTTGTATATCAITTCATTTATATATCAITTAGGTGCCATTTGG 752
Qy 678 GTTCTTTAAGAACTTGGCAATTTGGAACCTTTGGCTTGGTGTATATCTTGTCTTATTTGGTGC 737
Db 753 CATTTTCAAGAAATGAAATTTGGAAGCTTGAATTTGGAGATTAATCTTGGCAATTTGGGC 812
Qy 738 CATATTTGCTGCAACAGATTCAGTATGTACACTGCGAGTTCTGAATCAAGACGAGACACC 797
Db 813 AATCTTCTCTGTACAGATTTCTGTATGACCTTACAAAGTGTCTTAATCAGGATGAAACACC 872
Qy 798 TTTGCTTTACAGTCTTGTATTTGGGAGAGGTTGTGAATGATGCAACGTCAGTCTTGTGT 857
Db 873 CTTATTTGACAGTCTAGTTTCTGGGAAAGTGTGTGAATGATGCGACATCTCTAGTTCT 932
Qy 858 CTTCAACGCGATTCAGAGCTTTGATCTCACTCACTAAACCAAGAGCTGCTTTTCATCT 917
Db 933 GTTCAATGCTATCCAGACCTTTGACATCTCATCATCGACACGGGCAAGCTATGAAAT 992
Qy 918 TCTTGAAGAACTTCTGTATTTGTTTCTCTTAAGTACCTTGTCTTGGTGTGCAACCGGTCT 977
Db 993 AGTTGAAACCTTCTATCTATCTTGTGCTCAAGCACTGCGCTAGGAGTTGCTGCTGCGCT 1052
Qy 978 GATAAGTGGCTATGTTATCAAGAGCTATCTTTGGAAGCACTCAACTGACCGAGAGGT 1037
Db 1053 ACTGAGCGGCTATATTTATTAAGAACTCTACTTTTGAAGGCATCTCACTGACCGGTGAGGT 1112
Qy 1038 TGCCCTTATGATCTTATGCGCTATCTTCTTATGCTTGTGAGCTTTTCCACTTTGAG 1097
Db 1113 TGTATATGATACTCATGCTTACTTCTTACTTACTTGTCTGATTAATCTTATTTAAG 1172
Qy 1098 CGGTATCTCTCACTGTGTTTCTTGTGTTATGTTGATGTCCCATTAACATGACCAATGT 1157
Db 1173 TGCAATCTCTCACTGTGTTTCTCTGGATCGTGTCTCACTACACCTGGCATAATGT 1232
Qy 1158 AACGGAGAGCTCAAGATTAACAACAAGCTACTTTGGAAGCACTCAACTGACCGGTGCGGA 1217
Db 1233 GACTGAGAGCTCGAGAGTCACTACCAAGCACTTTTGTGTACATTAATCAATTTATGCTGA 1292
Qy 1218 GACATTTATTTCTGTATGTTTGGATGAGTCTTGGACATTCAGAGTGAATCCGT 1277
Db 1293 AATATTCATATCTTTATGTTGTTGATGATGTTTGGACATTTGAGAGTGGAGTTGT 1352
Qy 1278 GAGTGACACACCGGAACTCGATCGAGTGAAGTCAATCTTAATGGGTCTGTCTATGT 1337
Db 1353 AAGCGACAGCGCTTGGAAATATCAGTTTCAAGTTAGTCAATATTTGCTGGGTCTGTTTGT 1412
Qy 1338 TGGAGAGAGCGGTTGCTCTTCCGTTATGCTTCTTCTATCTTAAGTACCAAGAGATCA 1397
Db 1413 TGGAGAGAGAGCAATTTGTTTCCCATTTGTCATTTGTCATTCGACCAAGAAACTCC 1472
Qy 1398 AAGCGAGAAATCAACTTTAAACATGAGGTTGTGATTTGGTGTCTGCTCATGAGAG 1457
Db 1473 AGGGGCAAAATTTAGTTTAAACAGAGGTTTACAAATATGTTGGGCTGGATATGAGAG 1532
Qy 1458 TGCTGTATCTATGGCTCTTGATCAACAAGTTTACAAGGCGCGGACACAGATGACG 1517
Db 1533 TGCGGTTCTATGGCCCTTGTCTTATATCAAGTTTACAGGGAGGTCACTCAGTTACG 1592
Qy 1518 CGGGAATGCAATCATGATCAGAGTACGATTAATCTGCTCTTTTATGCAAGTGTGT 1577
Db 1593 CGCAATGCAATTAATGATCAAGTACTATCACTGTGTGCTTTTTCAGCAAGTGTGT 1652
Qy 1578 TGTATGCTGACCAACCACTCAT---AAGTCACTTATTACCGCACAGACGCCACAC 1634
Db 1653 TGGTTGATGACAAAACCTTTGATTAAGATATTTGCTACCTCTACAAACACTTTGAGCAG 1712
Qy 1635 GAGCATGTTATCTGATGACAAACCCCAAAATCCATACATATCCCTTTTGTGACCAAGA 1694
Db 1713 AATGATCTCTTCTGAACCAAGACCCCAAAATCTTCAATTTGTGCCACTCTTTCAGAGCAG 1772
Qy 1695 CTCGTTTCAATGAGCCCTTCAAGGAAACCAATATGTCCTCGGCCCTGACAGTATACGTGGT 1754

Db 1773 ACAGACTCAGAAAGCTGATCTGGAACGCCATGTATACCCGTCGCCACAGTTTGGGATGCT 1832
Qy 1755 CTTGACACGGCCCACTCGAACCGTGCATTTACTACTGGAGACAATTTGATGACTCTTTCAT 1814
Db 1833 CTTTTCAACCCCATCTCTATACAGTGCATTTACTTGAGAAAGTTTGACAATGCAATTCAT 1892
Qy 1815 GCGACCCGCTTTTGGAGGTCGTGGCTTTGTACCCCTTTGTTCAGGTTCTTCCAACCTGA 1871
Db 1893 GCGTCCAGTTTTCGGTGGAGCGAGGTTTGTACCTTTTGTCTCCAGGATCACCCGACAG 1949

RESULT 3
US-09-830-123-1
; Sequence 1, Application US/09830123
; Patent No. 6803500
; GENERAL INFORMATION:
; APPLICANT: Iida, Shigeru
; APPLICANT: Tanaka, Sachiko
; APPLICANT: Inagaki, Yoshihige
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles
; FILE REFERENCE: 001560-397
; CURRENT APPLICATION NUMBER: US/09/830,123
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/JP00/05722
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: JP 11/236800
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ. ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ. ID NO 1
; LENGTH: 2237
; TYPE: DNA
; ORGANISM: Ipomoea nil
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: (1)..(2237)
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the pH of vacuoles
; OTHER INFORMATION: pH of vacuoles
US-09-830-123-1

Query Match 35.6%; Score 774.8; DB 4; Length 2237;
Best Local Similarity 69.2%; Pred. No. 1.3e-187;
Matches 1096; Conservative 0; Mismatches 467; Indels 21; Gaps 2;
Qy 319 TTATCGACATCTGATCAGCGCTTCTGTGGTTGGCTTGAATCTCTTTGTGCACTTCTTTGT 378
Db 339 TTGTTCCAGCTGATCATGCTTCCGTTGTGTCGATGAACCTCTTTGTGGCGTTGCTTGC 398
Qy 379 GCTTGTATTTGCTTGTGTCATCTTTTGGAGAGATAGATGGATGAACGATCCATCACC 438
Db 399 GCATGCAATTTCTTTGGCCATCTACTCGAGGAGATCGCTGGGTGAACGAATCCATTTACT 458
Qy 439 GCTTGTTCATTTGGGCTAGGCACTGCTGTATACATTTTGTGATTAAGTAAAGGAAAAAGC 498
Db 459 GCCTTTAATTTGGTTTGTGACCGGAGTTGAATTTTGTCTCTTAGCGGAGGAAAGAGT 518
Qy 499 TCGCATCTTCTCGTCTTTTAGTGAAGATCTTTTCTCATATATCTTTTGCACCCCATTTATA 558
Db 519 TCACATCTTCTCGTCTTTTAGCGAAGATCTTTCTTTATATATCTCTCGCCACCTATAATA 578
Qy 559 TTCAATGCAAGGTTTCAAGTAAAGAGAGAGTTTTTCGCGCAATTTCTGATCATTTATG 618
Db 579 TTCAATGCGGGGTTTCAAGTGAAGAGAGAGTTTTTCGTGAACCTTCATGCAATTTATG 638
Qy 619 CTTTTTGGTGTGGGACTATTTCTTCACAATCATATCTCTAGGTGTAACACAG 678
Db 639 CTGTTTGGAGCTATTGGCACACTTATTAGCTGTTCTTATATATCATTTGTGGCGGTCAAA 698
Qy 679 TTCTTTAAGAAAGTTGGACATTTGAACTTTGACTTTGGGTGATTTATCTTGTATTTGTGTC 738
Db 699 ATTTTCAGCACTTAGACATTTGACTTTCTGGATTTTGGAGATTTATTAGCAATTTGTGCG 758
Qy 739 ATATTTGTGCAACAGATTCAGTATGTATGACACTGCGAGGTTCTGAAATCAAGACGAGACACT 798

Db 759 ATATTGCTGCAACCGGATCTGTTTGCACATTCAGGTGCTCAGTCAGGATGAGCGCC 818
Qy 799 TTGCTTTACAGCTCTGTTATTCGGAGAGGGTCTGTAATGATGCAACGTCAGTTGGTC 858
Db 819 CTACTTTACAGCTCTGTTGTAAGAGGGTCTCAATGATGTACTCTGTGGTCCCT 878
Qy 859 TTCAACCGGATTCAGAGCTTTGATCTCACTCACCTAAACCAACGAGCTGCTTTTCATCTT 918
Db 879 TTTAATGCTATTCAAGTTTGGACATGACTAGTTTGTATCCAAAAATTTGGCTTCATTC 938
Qy 919 CTGGAACCTCTGTAATTTGTTCTCTAAGTACCTTGTGTCGTGCTGCAACCGGTCTG 978
Db 939 ATTGGAACCTCTGTAATTTGTTCTCTCGAGCACTTTTGGGCGTGGGAATTTGCACTG 998
Qy 979 ATAAGTCGTATGTTATCAAGAGCTACTTTTGAAGGCACTCAACTGACCGGAGGTT 1038
Db 999 CTTTGTGCTATATATCAAAAGCTATCTTTGGAGGCACTCAACGATCGTAGGTT 1058
Qy 1039 GCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTCTGAGCTTTTCGACTTGAGC 1098
Db 1059 GCCCTTATGATGCTATGCTTACTTCTTATATATGATGCGGAGTTTATCTATCAAGC 1118
Qy 1099 GGTATCTCTACTGTTTCTGTTGTTGTAATGTCATGTCCTTACATGCGCAATGTA 1158
Db 1119 GGCATCTTACTGTTATCTTCTGTGGAATTTGTCAATGCTCAATATACCTGCGCAATGTT 1178
Qy 1159 ACGGAGAGCTCAAGATAACAAAGCACTACTTTTGAAGGCACTCAACTTTCATTTCTGGGAG 1218
Db 1179 ACGGAGAGCTCAAGGTCATCTAGGCACTCTTTTGAAGGCACTCAACTTTCATTTCTGGAG 1238
Qy 1219 ACATTTATTTCTTGTATGTTGAATGATGCTTGGACATTTGCAAGTGGAGATCCGTG 1278
Db 1239 ACATTTATCTCTATGTTGTTGATGATGCTTGGATATCGAGAAATGGAATTTGTG 1298
Qy 1279 AGTGACACCGGAGACATCGATGCGAGTCACTCAATCTAATGGTCTGGTCATGGTT 1338
Db 1299 AAAAAATAGTCAGGAGCTATCAGTTGTCAGTGAAGTCAATATGTTAGGCTCAATCTTAGTA 1358
Qy 1339 GGAAGAGCAGCTTCTGTTTCTGTTTCTATCTAATCTTAACTTAGCAAGAGATCAA 1398
Db 1359 GGCAGAGCTGGTTCGTTATCTTCTGTTTCTGTTTATCCACTTAGCAAGAAACTCT 1418
Qy 1399 AGCGAGAAATCAACTTTTAACTGAGGTTGTAATGTTGTTGTTGTTGTTGTTGTTGTTGTT 1458
Db 1419 TCGGACAAGATATCTTTTAGGCAACAAATAATTTTGGTGGCTGGCTTAATGAGAGC 1478
Qy 1459 GCTGTATCTATGCTCTTGATACAAAGTTTACAGGGCCGGGACACAGATGATGACG 1518
Db 1479 GCCGTCTCAATAGCACTTGGTATATAAGTTTACAACTCGGGGATACGTCATTGGAC 1538
Qy 1519 GGAATGCAATCATGATCAGAGTACGATAACTGCTGTTCTTTTACGACAGTGGTGT 1578
Db 1539 GAGAAGCAATATGATTAACAAGTACTGTTACGGTTGTTCTGTTACGACAGTGTATTC 1598
Qy 1579 GGTATGTCACAAACCACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1638
Db 1599 GGGTTGATGAGGAGCTCTGTAATAACCTTCTGTAACCTTCTGTAACCTTCTGTAACCTTCTGTA 1658
Qy 1639 -----ATGTTATCTGATGACAAACCCCAAAATCCATATCATATCCCTT 1683
Db 1659 GGTCAATGATGACAACTCCGAACCCAGTAGTCCGAAGCACTTCCAGGTGCCACTC 1718
Qy 1684 TTGGACCAA-----GACTCGTTCAATGAGCCTTTCAGGGAACCAAAATGCTCGGCT 1737
Db 1719 CTGGAACAAACCACTGACTCAGAAAGCATATGATAACCGGACCTGAGGTGCTCGACCA 1778
Qy 1738 GACAGTATAGTGGCTCTTTTGACACCGGCCATCTGGAACCGTGCATTAATCTAGTGAGACAA 1797
Db 1779 ACTGCCCTGGCATGCTGCTAAGGAGCGCAACCCCAACCGCTGACCGCTACTGGGCTAG 1838
Qy 1798 TTTGATGACTCTCTTATGAGACCGCTTCTGAGGTCGTGGCTTTGTATCCCTTTGTTC 1857

Db 1839 TTTGATGATTCGTTTATGCTCCGTTGTTGGCGGGGATTCGTTCCGTTTGTGCG 1898
Qy 1858 GGTCTCTCCAACTCAGAGAAACCT 1881
Db 1899 GGCTCACCAGTTGAGCAGAGCCCT 1922

RESULT 4
US-09-830-123-18
; Sequence 18, Application US/09830123
; Patent No. 6803500
; GENERAL INFORMATION:
; APPLICANT: Iida, Shigeru
; APPLICANT: Tanaka, Sachiko
; APPLICANT: Inagaki, Yoshihiko
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles
; FILE REFERENCE: 001560-397
; CURRENT APPLICATION NUMBER: US/09/830,123
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/JP00/05722
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: JP 11/236800
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 2361
; TYPE: DNA
; ORGANISM: Torenia hybrida
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(2361)
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the pH of vacuoles
; OTHER INFORMATION: pH of vacuoles
US-09-830-123-18

Query Match 34.6%; Score 754.4; DB 4; Length 2361;
Best Local Similarity 68.4%; Pred. No. 2.2e-182;
Matches 1090; Conservative 0; Mismatches 471; Indels 33; Gaps 2;

Qy 319 TTATCGACATCTGATCAGCTCTCTGTTGGTGGTGAATCTCTTTGTCACCTCTTTGT 378
Db 444 TTGTGGAGCTCTGTCACGGTTTCAGTGGTCGTATTAATCTTATTTGTCACCTCTCTCTGC 503
Qy 379 GCTTGTATTTCTTGTGTCATCTTTTGAAGAGATAGATGATGAACGAATCCATCACC 438
Db 504 ACACTATAGTATGTTGTCATCTCTCGAGGAAACCTTGGATGAATGATCTATCAT 563
Qy 439 GCTTGTGATGGCTAGGCACTGCTGTTACCAATTTTGTGATTAAGAAAGGAAAAAGC 498
Db 564 GCCCTCATAATTTGTTAGCCACGGAGTTATATCTCTGTTAATAGTGGTGGAAAAAGC 623
Qy 499 TCGCATCTTCGCTTTTAGTGAAGATCTTTTCTCATATATCTTTTGGCACCATTATA 558
Db 624 TCCCATCTCTTGGTGTTCAGTGAAGATCTTTTCTCATCTATGCGCTGCCACCAATCAT 683
Qy 559 TTCAATGACGGGTTTCAAGTAAAAAGAACGAGTTTTCGCAATTTCTGTCATTAATG 618
Db 684 TTTAATGCGGGTCCCAAGTAAGAAAGAAATCAATCTTTCGCAATTTTCGCACTATAATG 743
Qy 619 CTTTGTGTCGTTGGGACATTAATTTCTTGGCAATCATCATCTCTAGGTGTAACAG 678
Db 744 ATGTTTGGAGCAGTTGGTACCTTGATATCTTTCATCATCATCTTCACTCGTACCAATTGCA 803
Qy 679 TTTTAAAGAGTTGGACATTTGGAACTTTGACTTTGGGTGATTAATCTTGTCTATTGGTCC 738
Db 804 TTTTCCCAAAATGAACATGAGA---CTTGGAGTTGGAGATTAATCTTGTCTATTGGAGCT 860
Qy 739 ATATTGTCGAACAGATTCAGTATGTACACTGCAAGTTCCTGAATCAAGACGAGACACT 798
Db 861 ATTTTGTCTCAACAGACTCAGTTTGCACATTAAGGTGCTTAAGCGAGGACGAAACCA 920
Qy 799 TTGCTTACAGCTCTTGTATTTCGGAGAGGGTGTGTGTAATGATGACACGTCAGTTGTGTC 858

Db 921 CTGTGTACAGTCTAGTGTGTTGGCGAGGGTGTGTAATGACCGGACTTCAGTGGTCCCTA 980
QY 859 TTCAACGCGATTACAGAGCTTGTATCTCACTCACTAAACACCAAGAGCTGCTTTTTCATCTT 918
Db 981 TTTAATGCGATACAGAACTTCGACCTGCCCTCATATGCTACTGCTAAAGCTTTTCGAGCTT 1040
QY 919 CTTGGAACCTCTTGTATTTTCTCTTAAGTACCTTGTGCTGCTGCAACCGTCTG 978
Db 1041 GTTGGAACTCTTTTATTTATTTGCTACAGCACTGTGCTGGTGTCTGACTGCTGATTG 1100
QY 979 ATAAGTGGCTATGTTATCAAGAGCTATCTTTTGAAGGCACTCAACTGACCGAGAGTT 1038
Db 1101 CTTAGTGCTATACATCAATAAAGAGCTCTATTTTGAAGGCACTCCACTGATCCGAGGTT 1160
QY 1039 GCCTTTATGATGCTTATGGGATCTTTCTTATATGCTGCTGAGCTTTTCGACTTGAGC 1098
Db 1161 GCCATATGATCTATGCTGCTATCTGCTGATATGTTAGTGAATATTCGATTTGAGC 1220
QY 1099 GGTATCCTCACTGCTGTTTTCTGTGTTATGCTGATGCTCCCATTTACATGGCAATGTA 1158
Db 1221 GGTATCCTCACTGCTGTTTTCTGTGAAATGCTGCTGCACTATACATGGCAATGTC 1280
QY 1159 ACGGAGCTCAAGATTAACAAAGCACTACCTTTTGCACCTTTGCTATTTCTTGGGAG 1218
Db 1281 ACTGAAGACTCAAGAGTTACCAAGCACTATATTTGCGACATTTGCTATTTGCTGAA 1340
QY 1219 ACATTTATTTCTGTATGTTGGAATGGAATGCACTTGCACATTCACAAGTGGAGATCCGTG 1278
Db 1341 ATATTTATTTCTGTATGTTGCAATGGAATGCTTTAGACATTCAGAAATGGAATTCGTA 1400
QY 1279 AGTGACACACCGGAAATCGATCGCAGTGAGCTCAATCCTAATGGGCTGCTGCTCATGGTT 1338
Db 1401 AGCGGAGCATGACAACTCGCAGCTGTCTGAGTCACTCTGCTGGGATTTGTTGCTC 1460
QY 1339 GGAAGAGCAGCTGCTGCTTCCGTTATCGTTTCTATCTAATCTTACCTAGCAGAAAGATCAA 1398
Db 1461 TCAAGAGCAGCTTGTATTTCCCTTTATCATTTCTCTCCAATCTGCGCAAAAGTCCCCA 1520
QY 1399 ACGGAAATCAACTTTAATGCAAGTGTGCTATTTGGTGGTCTGCTCATGAGAGT 1458
Db 1521 CTCGAAATCACTAGTCTCAGGAGCAAAATATATATGTTGGTGGTCTTATGCGCGGA 1580
QY 1459 GCTGTATCTATGCTCTTGATACAAAGTGTATACAGGCGCGGCAACAGATGTACGC 1518
Db 1581 GCGTTTCCATGCTCTGCTTACAGCAGTTTACTAGAGAGGTCTCACAGTGGAAAGT 1640
QY 1519 GGAATGCAATCATGATCAGAGTACGATTAATGCTGCTGCTTTTATGACAGTGGTGT 1578
Db 1641 GAAATGCCATATTCATCACAGTACAAATCACCAATGCTGCTTTCAGCACTGTGGTGT 1700
QY 1579 GGTATGCTGACCAACCACTATAGCTACCTATATACCGCACAGAACGCCACCGAGC 1638
Db 1701 GGTATGATGACGAAGCGCTTCATCAATTTACTGATACCTTCACCAAGCTTAAAGATCG 1760
QY 1639 ATGTTATCTGATGACAAACCCCAAAATCCATACATATCCCTTTGTTGACCAAGACTCG 1698
Db 1761 GTCTCTCAGAACCGTGAATCCAACTCCATCACATCCCACTCTCGGGAAAGTCAG 1820
QY 1699 TTCAITGAGCTTC-----AGGAAACCAATGTG 1728
Db 1821 GACTCTGTGGCCGAACTATTTCAGCATCAGAGTCAAACTTTCAAGAGTGGCGCAACCGTT 1880
QY 1729 CTTGCGCTGACAGTATAGTGGCTTCTTGACAGCGGCCCACTCGAACCGGTGCTACTAC 1788
Db 1881 GCTGACCGAGCAGCTACGATGTTACTCACAAAGCCCACTCATACGGTGCATATAT 1940
QY 1789 TGGAGACAATTTGATGACTCTTTCATGCGACCGCTCTTTGGAGGCTGCTGCTTTGTACCC 1848
Db 1941 TGGAGAAATTCAGCAATGCTTTTATGCGTCCGCTCTTTGTTGGGCTGCTTTGTACCA 2000
QY 1849 TTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTC 1882

Db 2001 TATGTTCCGGTTTACCAGACTGAACGAAGGTTTC 2034
RESULT 5
US-09-800-729-22
; Sequence 22, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044PI
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 22
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (959)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1565)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-22

Query Match 4.2%; Score 91.2; DB 4; Length 1581;
Best Local Similarity 47.6%; Pred. No. 3.8e-13;
Matches 369; Conservative 6; Mismatches 370; Indels 30; Gaps 3;

QY 522 AGATCTTTTTCATATATCTTTTGGCCACCCCATATATTAATCAATGACAGGGTTTCAAGTAAA 581
Db 433 AGAAGTATTTTCAACATTTCTTCTGCTCCAAATATTTTTCATGCTGGATACAGCTTAAA 492
QY 582 AAAGAGCAGTGTTCGCAATTTTCGTGACTATATATGCTTTTGGTGTGTTGGGACTAT 641
Db 493 GAAGAGACACTTTTTCAGAAATCTTGGATCTATACCTGCTATGCTTCTTGGGACTGC 552
QY 642 TATTTCTTGCAATCATATCTCTAGGTGTAAACAGTGTCTTTTAAAGAGTTGGACATT-- 699
Db 553 TGKTTTCATGCTTCAITTTTGGAAATCTCATGTATGCTGTGGTGAAGCTCATGAAGATTAT 612
QY 700 -----GGAACTTTGACTTGGTGGTATATCTTGTATTTGGTGCCATATTTGC 746
Db 613 GGGACAGCTCTCAGATAAAATTTTACTACAGAAATGCTCTTTTGGAGCAATCATCTC 672
QY 747 TGCAACAGATTCAGTATGTACACTGCAGGTTCTTGAATCAAGACGACAGACCTTTTG--CT 803
Db 673 TGCCACTGACCGAGTGTGCTGGCGATATTTAATGAATTCATGTCAGACGCTGGATCT 732
QY 804 TTACAGTCTTGTATTCGGAGAGGTTGTGTGAATGATGCAACGTCAGTTGTGTCTTCAA 863
Db 733 TTACGCACTTCTTTTGGAGAGAGCGTCTCTAAATGATGCTTTTGGCCATTTGKACTGKCTC 792
QY 864 CGCGATTTCAGAGCTTTGATCTCACTCACTAAACACGAGGCTGCTTTTTCATCTTCTTGG 923
Db 793 GTCATTTGTTGCTTACCAGCGGAGCTGAACACTCAGCCTTTGATGCTGCTGCTGCTT 852
QY 924 AAACTTCTTGTATTTGTTTCTCTTAAGTACCTTTGCTTGGTGTGCAACCGGCTGTAAAG 983
Db 853 TTTAAGTCAGTTGGCAITTTTCTAGGTATATTTAGTGGCTCTTTTACCATGGAGCTGT 912
QY 984 TCGGTATGTTA-----TCAAGAGCTATATCTTTTGGAGGCACTCAACTGACCG 1031

Db 471 TTTGATCCAGAGTATTTTCAACATATTTACCTTCCTCATATATTTATGACAGTTAT 530
Qy 574 CAAAGTAAAGAGAGAGTATTTTCCCAATTTTCGTGACTATTTATGCTTTTGTGCTGT 633
Db 531 AGCCTGAAAGAGAGAGATTTTTCGAAATCTTGGGTCTATCTAGCATACGCTTTTCTT 590
Qy 634 GGGACTATTTATTTCTTGCA-----CAATCATATCTAGGTGTAACACAGTTC 681
Db 591 GGAACAGCAATTTCTTGTTCGTTATTTGGTCAATAATGATGGCTGTGTAACGCTGATG 650
Qy 682 TTTAAGAGTTGACATTT---GGAACCTTTGACTTGGGTGATTTATCTTGTATTTGTGTC 738
Db 651 AAGGTAACGGGACAACTTCGAGAGATTTTACTTTACAGATGCTTACTGTTTGTGTC 710
Qy 739 ATATTTGCTGCAACAGATTCAGTATGATACATGCTGAGGTTCTGAATCAAGACGAGACCT 798
Db 711 ATTGATATCAGCAACTGATCAGTGACTGTTCTTGCTATATTTCCAGAGCTTCAAGTTGAT 770
Qy 799 TTG---CTTTACAGTCTTGTATTCGAGAGGTTGTTGTGATGATCAAGCTCAGTTGTC 855
Db 771 GTTGAACCTATGCACTTCTTTTGGTGAAGTGTCTCAATGATGCTGTGTCATAGTG 830
Qy 856 GTCTTCAACGGGATTCAGAGCTTTGATCTCACTCACTAAAC-----CAC 900
Db 831 CTGTCTCTCAATAGTGGCATACCAAGCAGCTGGAGACAAAGTCACACCTTTGATGTC 890
Qy 901 GAAGCTGCTTTTTCATCTTCTTGGAACTTCTTGTATTTTGTCTTCTCAAGTACCTTGTCT 960
Db 891 ACAGCGATGTTCAAGTCTATTTGGATCTTCTTGGATCTTCAAGTGAATCTTTTGCATG 950
Qy 961 GGTGCTGCAACCGGCTCTGATAAGTGGTATGTTATCAAGAGCTATATTTTGAAGGCAC 1020
Db 951 GGTGCTGCTACTGAGTGGTGACAGCTTTAGTGACAAAGTTACCAAAATTT---ACGGGAG 1007
Qy 1021 TCAACTGACCGAGAGTGGCTTATGATGCTTATGCGCTATCTTCTTATATGCTTGTCT 1080
Db 1008 TTCCAGTGTGGAGACAGGCTTGTCTTCTGATGCTCTGGAGTACCTTCTCTTGGCT 1067
Qy 1081 GAGCTTTTTCGACTTGACGGTATCTCTCACTGTGTTTTTCTGTGATTTGTGATGCTCCAT 1140
Db 1068 GAAGCATGGGCTTTCAGGTGTAGTTGAGTATGTTTGTGGCATCACAAAGCACAT 1127
Qy 1141 TACATATGGCAGATGTAACGGAGAGCTCAAGATAACAAAGACATATCTTTGCAACT 1200
Db 1128 TATACGTATAAATTTTGTCCAGAGTCTCAGCATAGAACTAAACAGTGTGTTGAGCTT 1187
Qy 1201 TTGTCATTTCTTGGCGAGACATTTATTTCTTGTATGTTGGAATG 1245
Db 1188 CTCAATTTCTTGGCAGAGAAATTTTCATCTTCTCTACATGGGGCTG 1232

RESULT 9

US-09-949-016-4129
; Sequence 4129, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4129
; LENGTH: 4460
; TYPE: DNA

; ORGANISM: Human
US-09-949-016-4129

Query Match 2.7%; Score 59.8; DB 4; Length 4460;
Best Local Similarity 47.6%; Pred. No. 6.1e-05;
Matches 364; Conservative 0; Mismatches 367; Indels 34; Gaps 5;

Qy 514 TTTAGTGAAGATCTTTTCTTCAATATATCTTTTGGCCACCCATATATTTCAATGACAGGTTT 573
Db 475 TTTGATCCAGAGTATTTTTCGAAATCTTGGGTCTATCTAGCATACGCTTTTCTT 534
Qy 574 CAAAGTAAAGAGAGAGTATTTTTCGCAATTTTCGTGACTATTTATGCTTTTGTGCTGT 633
Db 535 AGCCTGAAAGAGAGAGATTTTTCGAAATCTTGGTCTATCTAGCATACGCTTTTCTT 594
Qy 634 GGGACTATTTATTTCTTGCA-----CAATCATATCTCTAGGTGTAACACAGTTC 681
Db 595 GGAACAGCAATTTCTTGTTCGTTATTTGGGTCAATAATGATGGCTGTGTAACGCTGATG 654
Qy 682 TTTAAGAGTTGACATTT---GGAACCTTTGACTTGGGTGATTTATCTTGTATTTGTGTC 738
Db 655 AAGGTAACGGGACAACTTCGAGAGATTTTACTTTACAGATTTGCCCTACTGTTTGTGTC 714
Qy 739 ATATTTGCTGCAACAGATTCAGTATGATCACTGACAGTTCCTGAATCAAGACGAGACACT 798
Db 715 ATTGATATCAGCAACTGATCCAGTGAATCTTGTGATATTTCCAGAGCTTCAAGTTGAT 774
Qy 799 TTG---CTTTACAGTCTTGTATTTTCGAGAGGTTTGTGTAAGTATGATCAAGCTCAGTTGT 855
Db 775 GTTGAACCTATGCACTTCTTTTGGTGAAGTGTCTCAATGATGCTGTGTCATAGTG 834
Qy 856 GTCTTCAACGGGATTCAGAGCTTTGATCTCACTCACTAAAC-----CAC 900
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Qy 901 GAAGCTGCTTTTCACTTCTTGGAACTTCTTGTATTTTCTCTCAAGTACCTTGTCTT 960
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Qy 961 GGTGCTGCAACCGGCTCTGATAAGTGGTATGTTATCAAGAAGCTATATTTTGAAGGCAC 1020
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Qy 1021 TCAACTGACCGAGAGTTCCTCTTATGATGCTTATGCGGTATTTGCGGTATCTTTATATGCTT 1080
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Qy 1081 GAGCTTTTTCGACTTGACGGTATCTCTCACTGTGTTTTTCTGTGATTTGTGATGCTCCAT 1140
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Db 1194 CTCAATTTCTTGGCAGAGAAATTTTCATCTTCTCTACATGGGGCTG 1238

RESULT 10

US-09-524-101D-5
; Sequence 5, Application US/09524101D
; Patent No. 6762291
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: INSECT P53 TUMOR SUPPRESSOR GENES AND PROTEINS
; FILE REFERENCE: EX00015C FIRST AMENDMENT
; CURRENT APPLICATION NUMBER: US/09/524,101D
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/268,969
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: US 60/184,373

Db 173 CGCTCTTCTTGAAGAACTGAACATAAATAATGTAATATGACGCCACATTTATTTATTT 114
Qy 2074 GTAATTATATTCATATTTGTTTGTGTAAACAAACTACACATTTGTTTATGTTTGA 2133
Db 113 GATATTATTACCATTCITTTGATCATATTTGCTTTTATTTTTCATTTTATTTTCA 54
Qy 2134 TTGGGTTTTGCTTCGAAAAAATTTTTATATATATATATATATATATATATATAT 2178
Db 53 AATATATATGTTTAT 9

RESULT 13
US-09-005-051-36
; Sequence 36, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: PC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11..1594
US-09-005-051-36

Query Match 2.5%; Score 53.8; DB 3; Length 2007;
Best Local Similarity 52.4%; Pred. No. 0.0015;
Matches 118; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

Qy 1954 AATATGCTTTTGTGTAATATTCATTTGTAATATTTGTTGAGGACAGAAATCTGT 2013
Db 1775 AACAAATTCGTTTGTAGTATTTGCGCATTCACAGATGCTGCTGCTAAATTTGT 1834
Qy 2014 CCTAACGTTTTTGAGACAGAAAGCAAAACATGCGCACTTTGAAAGTGTGTTGATGATGTAT 2073
Db 1835 CGCTCTTCTTGAAGAACTGAACATAAATAATGTAATATGACGCCACATTTATTTATTT 1894
Qy 2074 GTAATTATATTCATATTTGTTTGTGTAAACAAACTACACATTTGTTTATGTTTGA 2133

Db 1895 GATATTATTACCATCTTTGATCATATTTGCTTTTATTTTTCATTTTATTTTCA 1954
Qy 2134 TTGGGTTTTGCTTCGAAAAAATTTTTATATATATATATATATATATATATATAT 2178
Db 1955 AATATATGTTTAT 1999

RESULT 14
US-09-005-051-38/c
; Sequence 38, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: PC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-005-051-38

Query Match 2.5%; Score 53.8; DB 3; Length 2007;
Best Local Similarity 52.4%; Pred. No. 0.0015;
Matches 118; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

Qy 1954 AATATGCTTTTGTGTAATATTCATTTGTAATATTTGTTGAGGACAGAAATCTGT 2013
Db 233 AACAAATTCGTTTGTAGTATTTGCGCATTCACAGATGCTGCTGCTAAATTTGT 174
Qy 2014 CCTAACGTTTTTGAGACAGAAAGCAAAACATGCGCACTTTGAAAGTGTGTTGATGATGTAT 2073
Db 173 CGCTCTTCTTGAAGAACTGAACATAAATAATGTAATATGACGCCACATTTATTTATTT 114
Qy 2074 GTAATTATATTCATATTTGTTTGTGTAAACAAACTACACATTTGTTTATGTTTGA 2133
Db 113 GATATTATTACCATCTTTGATCATATTTGCTTTTATTTTTCATTTTATTTTCA 54
Qy 2134 TTGGGTTTTGCTTCGAAAAAATTTTTATATATATATATATATATATATATATAT 2178
Db 53 AATATATGTTTAT 9

RESULT 15
US-09-403-942F-36
; Sequence 36, Application US/09403942F
; Patent No. 6664090
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary M.
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: NOVEL CARBOXYLESTERASE NUCLEIC ACID MOLECULES, PROTEINS AND USES
; FILE REFERENCE: FC-1-CI-PUS
; CURRENT APPLICATION NUMBER: US/09/403,942F
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US97/20598
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/747,221
; PRIOR FILING DATE: 1996-11-12
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(1594)
; OTHER INFORMATION:
US-09-403-942F-36

Query Match 2.5%; Score 53.8; DB 4; Length 2007;
Best Local Similarity 52.4%; Pred. No. 0.0015;
Matches 118; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

| | | | |
|----|------|---|------|
| Qy | 1954 | AAATTATGCTTTTGTGTAATTTATCCATTTTGTAAATTTTGTGAGGACAGAAATCTGT | 2013 |
| Db | 1775 | ACAAATTCGTGTTTGTGTAATTTATCCATTTTGTAAATTTTGTGAGGACAGAAATCTGT | 1834 |
| Qy | 2014 | CCTAACGTTTGTGAGACAGAAAGCAAAACATGGCACTTTGAAAGTGTGATTGATGAT | 2073 |
| Db | 1835 | CGCTCTTCTTGAAGAACTGAACATAAATGTAATTAATGACGCCACATTTATATTT | 1894 |
| Qy | 2074 | GTAATTAATTCATATTTGTTGTTGTAACAACTACACATTTGTTTATGTTTGA | 2133 |
| Db | 1895 | GATATTATTAACATCTTTGTTGTTGTAACAACTACACATTTGTTTATGTTTGA | 1954 |
| Qy | 2134 | TTTGGTTTTCCTCGAAAAAATAAAAAAAAAAAAAAAAAAAAAA | 2178 |
| Db | 1955 | AATATATTGTTTATTAATAAAAAAAAAAAAAAAAAAAAAA | 1999 |

Search completed: April 26, 2005, 08:45:17
Job time : 396 secs

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 02:22:21 ; Search time 1194 Seconds

(without alignments)
10798.322 Million cell updates/sec

Title: US-10-617-623-1

Perfect score: 2178
Sequence: 1 cctctgttcttctctcg.....aaaaaaaaaaaaaaaaaaaaa 2178

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 2178 | 100.0 | 2178 | 2 | Aaz22591 Arabidops |
| 2 | 2143.4 | 98.4 | 2284 | 2 | Aaz22595 Arabidops |
| 3 | 1617 | 74.2 | 1617 | 6 | Abz13434 Arabidops |
| 4 | 1617 | 74.2 | 1617 | 12 | Adn74230 Thale cre |
| 5 | 1614 | 74.1 | 1614 | 12 | Adn11979 Wild type |
| 6 | 1612.4 | 74.0 | 1614 | 12 | Adn11981 AtHNX1 mu |
| 7 | 1563 | 71.8 | 1563 | 12 | Adn11983 AtHNX1 mu |
| 8 | 1563 | 71.8 | 1566 | 12 | Adn11989 NDL-1 enc |
| 9 | 1473 | 67.6 | 1473 | 12 | Adn11985 AtHNX1 mu |
| 10 | 1407 | 64.6 | 1410 | 12 | Adn11991 NDL-2 enc |
| 11 | 1362 | 62.5 | 1362 | 12 | Adn11987 AtHNX1 mu |
| 12 | 1320.4 | 60.6 | 1323 | 12 | Adn11993 NDL-3 enc |
| 13 | 848 | 38.9 | 1449 | 12 | Adm68265 Plant Na+ |
| 14 | 832.8 | 38.2 | 1668 | 3 | Aaa72926 AtLiplex |
| 15 | 821.2 | 37.7 | 2553 | 4 | Aaf75765 Gene regu |
| 16 | 813 | 37.3 | 2423 | 4 | Aaf75764 Gene regu |
| 17 | 806.4 | 37.0 | 1668 | 6 | Acc49921 Suaeda sa |
| 18 | 806.4 | 37.0 | 2397 | 6 | Acc49920 Suaeda sa |
| 19 | 805.4 | 37.0 | 1315 | 12 | Adm68266 Arabidops |
| 20 | 797.6 | 36.6 | 1620 | 10 | Adj99891 Potato sa |

| | | | | | |
|----|-------|------|------|----|--------------------|
| 21 | 794.4 | 36.5 | 1621 | 10 | Adj99890 |
| 22 | 774.8 | 35.6 | 2237 | 4 | Aaf75752 Gene regu |
| 23 | 768.8 | 35.3 | 2330 | 3 | Aaa61876 cDNA enco |
| 24 | 754.4 | 34.6 | 2361 | 4 | Aaf75766 Gene regu |
| 25 | 682.6 | 31.3 | 1638 | 10 | ACF58165 |
| 26 | 651 | 29.9 | 1955 | 11 | ADM82830 |
| 27 | 523.8 | 24.0 | 1788 | 2 | Aaz22592 Arabidops |
| 28 | 491.6 | 22.6 | 1674 | 6 | ABK12638 DNA encod |
| 29 | 418 | 19.2 | 418 | 8 | ABX62293 Arabidops |
| 30 | 401.8 | 18.4 | 1740 | 12 | ADM68263 Mangrove |
| 31 | 269.2 | 12.4 | 612 | 13 | ACN53419 Cotton an |
| 32 | 252.6 | 11.6 | 330 | 2 | Aaz22611 Arabidops |
| 33 | 226.4 | 10.4 | 378 | 2 | Aaz22606 Rice Na/H |
| 34 | 191 | 8.8 | 613 | 10 | ADD17688 DNA (Seq1 |
| 35 | 165.2 | 7.6 | 466 | 12 | ADP94869 Cotton ex |
| 36 | 165.2 | 7.6 | 466 | 13 | ADR62082 Cotton cD |
| 37 | 153.2 | 7.0 | 588 | 10 | ADD17689 DNA (Seq1 |
| 38 | 152.2 | 7.0 | 573 | 13 | ACN47580 Cotton pr |
| 39 | 149.4 | 6.9 | 596 | 13 | ACN60354 Cotton pr |
| 40 | 146.4 | 6.7 | 2000 | 6 | ABZ16128 Arabidops |
| 41 | 141.8 | 6.5 | 1824 | 3 | AAC95373 Cat flea |
| 42 | 141.8 | 6.5 | 1824 | 3 | AAC95372 Cat flea |
| 43 | 141.8 | 6.5 | 2080 | 3 | AAC95370 Cat flea |
| 44 | 141.8 | 6.5 | 2080 | 3 | AAC95371 Cat flea |
| 45 | 125 | 5.7 | 281 | 6 | ABL73323 Corn tass |

ALIGNMENTS

RESULT 1
Aaz22591
ID AAZ22591 standard; cDNA; 2178 BP.

XX AAZ22591;

DT 18-JAN-2000 (first entry)

DE Arabidopsis thaliana Na/H transporter gene AtNHX1.

XX Sodium; proton; antiport; transporter; salt tolerance; salt management;
KW transgenic plant; survival; soil; farming; accumulation; irrigation;
KW crop; ss.

OS Arabidopsis thaliana.

PN WO9947679-A2.

XX 23-SEP-1999.

PF 18-MAR-1999; 99WO-CA000219.

PR 18-MAR-1998; 98US-0078474P.

PR 15-JAN-1999; 99US-011611P.

XX (BLUM/) BLUMWALD E.

PA (APSE/) APSE M.

PA (SNED/) SNEDDEN W.

PA (AHAR/) AHARON G.

XX Blumwald E.; Apse M, Snedden W, Aharon G;

XX WPI; 1999-571840/48.

XX P-PSDB; AAY40901.

XX Nucleic acid molecules encoding sodium/proton transport polypeptides,
XX useful in genetic engineering salt tolerance in crop plants.

XX Claim 4; Fig 1A; 93pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a
XX plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and
XX capable of increasing salt tolerance in a cell. This sequence corresponds

CC to the gene encoding the AtNHX1 transporter from *Arabidopsis thaliana*.
 CC The Na/H transporter polypeptides provide a means of intracellular salt
 CC management, particularly in plants. The sequences are useful for
 CC producing transgenic plants that are capable of surviving in soil with
 CC high salt levels that would normally inhibit growth of the crop species.
 CC This would be useful in farming land in areas that are generally
 CC considered unproductive through salt accumulation and poor irrigation,
 CC e.g. in India, Australia, and prairies in USA or Canada. Commercial
 CC crops, such as spinach, tomatoes, brassica, cotton, sunflower,
 CC strawberries, spinaches, lettuce, rice, soybean, corn, wheat, rye, barley,
 CC atriplex, sorghum, alfalfa, salicornia and others would benefit from
 CC increased salt tolerance
 XX

SQ Sequence 2178 BP; 576 A; 413 C; 472 G; 717 T; 0 U; 0 Other;

Query Match 100.0%; Score 2178; DB 2; Length 2178;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCTCTGTTTCGTTCTCGTAGCAAGAAAGAAATCTCAGGTTTTCGATTCGA 60
DB 1 CCTCTGTTTCGTTCTCGTAGCAAGAAAGAAATCTCAGGTTTTCGATTCGA 60

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DB 61 AGCTTCCAAAATTTGAATTTGATCTCTCTGGGCTCTTTTGTAAATCAGACTGAGATAT 120

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DB 121 TTAGATTACCCAGAAAGTTGTTCAAGGAATGTTTTCAGTGACAGCAGCGGAAGATAAAG 180

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DB 181 AGACTTTTTTTTTCAGATTTTTCGATCCAAAATCTCAATAGTTGTTTTCATGTTCTTGGAT 240

QY 241 CAAATCTGGAAGAGGAGTTGTTGGATCTAGCAAGATAAATGTTGGATTTCTCTA 300
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QY 301 GTGTCCAAAATCGCTTCTGTTATCGACATCTGATCAAGCTTCTGTTGGTTGTAATCTC 360
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DB 421 ATCAACGAATCCATCACCGCTTGTGATTTGGCTAGGCACCTGTTTACCATTTTGTG 480

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DB 541 CTTTTCGCCACCAATTATATCAATGAGGTTTCAAGTAAAGAAAGAGAGTTTTCGCG 600

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DB 781 AATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTTCGGAGAGGCTTCTGTGAATGAT 840

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DB 1441 TCTGCTCTCATGAGAGGTTGTTATCTATGCTCTTGCATACAAACAAGTTTACAAAGGCC 1500
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DB 1801 GATGATCTCTTTCATGACCGCTCTTTTGGAGGTCGTGGCTTGTGACCCCTTTGTTCCAGGT 1860
QY 1861 TCTCCAACTGAGAGAAAACCTCTCTGATCTTTAGTAAAGCTTGGAGGTAACCTGGAAGAAA 1920
DB 1861 TCTCCAACTGAGAGAAAACCTCTCTGATCTTTAGTAAAGCTTGGAGGTAACCTGGAAGAAA 1920

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346 GTTGGTGTGAATCTCTTTGTTGCACTTCTTTGTGCTTGATTTGTTCTTGGTCACTTTTG 405
Db |||||
61 GTTGGTGTGAATCTCTTTGTTGCACTTCTTTGTGCTTGATTTGTTCTTGGTCACTTTTG 120
Qy |||||
406 GAAGAAATAGATGATGAACCAATCCATCACCGCTTGTGTTGATTTGGGCTTAGGCACTGGT 465
Db |||||
121 GAAGAAATAGATGATGAACCAATCCATCACCGCTTGTGTTGATTTGGGCTTAGGCACTGGT 180
Qy |||||
466 GTTACCAATTTGTTGATTAAGAGAAAGCTCGCATCTTCTGCTTTTGTAGTGAAGAT 525
Db |||||
181 GTTACCAATTTGTTGATTAAGAGAAAGCTCGCATCTTCTGCTTTTGTAGTGAAGAT 240
Qy |||||
526 CTTTCTTCATATATCTTTTGCACCAATTAATTAATGCGAGGTTTCAAGTAAAAAG 585
Db |||||
241 CTTTCTTCATATATCTTTTGCACCAATTAATTAATGCGAGGTTTCAAGTAAAAAG 300
Qy |||||
586 AAGCAGTTTTCGCAATTTCTGAGCTATTATGCTTTTGGTCTGTTGGGACTATTATT 645
Db |||||
301 AAGCAGTTTTCGCAATTTCTGAGCTATTATGCTTTTGGTCTGTTGGGACTATTATT 360
Qy |||||
646 TCTTGCACAATCATATCTCTAGGTGAACAAGTCTTTTAAGAAAGTTGGACATTTGAACC 705
Db |||||
361 TCTTGCACAATCATATCTCTAGGTGAACAAGTCTTTTAAGAAAGTTGGACATTTGAACC 420
Qy |||||
706 TTTGACTTGGTGATTAATCTGCTATTTGTCGCAATTTGCTGCAACAGATTCAGTATGT 765
Db |||||
421 TTTGACTTGGTGATTAATCTGCTATTTGTCGCAATTTGCTGCAACAGATTCAGTATGT 480
Qy |||||
766 ACACTGCAAGTCTGAAATCAAGACGAGACACCTTTGCTTTACAGTCTTGTATTCGAGAG 825
Db |||||
481 ACACTGCAAGTCTGAAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTCGAGAG 540
Qy |||||
826 GGTGTTGTGAATGATCAAGCTCAGTTGTGCTTCAACGCGATTCAGAGCTTTTGATCTC 885
Db |||||
541 GGTGTTGTGAATGATCAAGCTCAGTTGTGCTTCAACGCGATTCAGAGCTTTTGATCTC 600
Qy |||||
886 ACTCAGCTAAACACGAGCTGCTTTTCACTTCTTTGGAAACCTTCTGTATTTGTTTCTC 945
Db |||||
601 ACTCAGCTAAACACGAGCTGCTTTTCACTTCTTTGGAAACCTTCTGTATTTGTTTCTC 660
Qy |||||
946 CTAAGTACCTTGTGCTGCTGCAACCGGCTGATAGTGAAGTCTGATCTATCAAGAGCTA 1005
Db |||||
661 CTAAGTACCTTGTGCTGCTGCAACCGGCTGATAGTGAAGTCTGATCTATCAAGAGCTA 720
Qy |||||
1006 TACTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTATGGCGTATCTT 1065
Db |||||
721 TACTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTATGGCGTATCTT 780
Qy |||||
1066 TCTTATATGCTTGTGCTGAGCTTTTTCGACTTGGAGCGGTATCTCACTGTGTTTCTGTGGT 1125
Db |||||
781 TCTTATATGCTTGTGCTGAGCTTTTTCGACTTGGAGCGGTATCTCACTGTGTTTCTGTGGT 840
Qy |||||
1126 ATTGTGATGCTCCATTTACATGCGCAATGTAACGGAGGCTCAAGATTAACAACAAG 1185
Db |||||
841 ATTGTGATGCTCCATTTACATGCGCAATGTAACGGAGGCTCAAGATTAACAACAAG 900
Qy |||||
1186 CATACCTTTGCACTTTGTTCATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 1245
Db |||||
901 CATACCTTTGCACTTTGTTCATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 960
Qy |||||
1246 GATGCTTTGGACATTCACAAAGTGGAGATCGGTGAGTGACACACCGGGAACATCGATCGCA 1305
Db |||||
961 GATGCTTTGGACATTCACAAAGTGGAGATCGGTGAGTGACACACCGGGAACATCGATCGCA 1020
Qy |||||
1306 GTGAGCTCAATCTAATGGTCTGCTCATGTTGGAAGACGCGTTCGTTTCCGTTA 1365
Db |||||
1021 GTGAGCTCAATCTAATGGTCTGCTCATGTTGGAAGACGCGTTCGTTTCCGTTA 1080
Qy |||||
1366 TCGTTTCTATCTAATCTAGCCAAAGAAATCAAGCGAGAAATCAACTTTTAACATGCGAG 1425
Db |||||
1081 TCGTTTCTATCTAATCTAGCCAAAGAAATCAAGCGAGAAATCAACTTTTAACATGCGAG 1140
Qy |||||
1426 GTTGTGATTTGGTGTCTGCTCTCATGAGAGGTGCTGTATCTATGCTCTTTCGCATACAAC 1485

1141 GTTGTGATTTGGTGGTCTGGTCTCATGAGAGGTGCTGTATCTATGCTCTTTCGCATACAAC 1200
Qy |||||
1486 AAGTTTACAAAGGCGCGGCGACACAGATGTACGCGGAATGCAATCATGATCACGAGTACG 1545
Db |||||
1201 AAGTTTACAAAGGCGCGGCGACACAGATGTACGCGGAATGCAATCATGATCACGAGTACG 1360
Qy |||||
1546 ATAACTGTCTGCTCTTTTATAGCAGTGGTGTGTTGTTGATGCTGACCAAAACCACTCATAAAC 1605
Db |||||
1261 ATAACTGTCTGCTCTTTTATAGCAGTGGTGTGTTGTTGATGCTGACCAAAACCACTCATAAAC 1320
Qy |||||
1606 TACCTATTACCCACACAGAACGCCACCGAGCATGTTATCTGATGACAAACACCCCAAAA 1665
Db |||||
1321 TACCTATTACCCACACAGAACGCCACCGAGCATGTTATCTGATGACAAACACCCCAAAA 1380
Qy |||||
1666 TCCATACATATCCCTTTTGTGGACCAAGACTCGTTCAATTGAGCCTTTCAGGGAACCACAAT 1725
Db |||||
1381 TCCATACATATCCCTTTTGTGGACCAAGACTCGTTCAATTGAGCCTTTCAGGGAACCACAAT 1440
Qy |||||
1726 GTGCTTCGCGCTGACAGTATAGTGGCTTCTTGACAGCGGCCCACTCGAACCGTGCATTAC 1785
Db |||||
1441 GTGCTTCGCGCTGACAGTATAGTGGCTTCTTGACAGCGGCCCACTCGAACCGTGCATTAC 1500
Qy |||||
1786 TACTGGAGACAATTTGATGACTCTTTCATGCGACCGCTCTTTGGAGGTCGTGGCTTTGTA 1845
Db |||||
1501 TACTGGAGACAATTTGATGACTCTTTCATGCGACCGCTCTTTGGAGGTCGTGGCTTTGTA 1560
Qy |||||
1846 CCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCTCTGATCTTATAGAGGCTTGA 1902
Db |||||
1561 CCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCTCTGATCTTATAGAGGCTTGA 1617

RESULT 4

ADN74230

ID ADN74230 standard; cDNA; 1617 bp.

XX ADN74230;

XX DT 15-JUL-2004 (first entry)

XX Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2125.

XX gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;

KW growth regulator; animal feed product; thale cress;

KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.

XX Arabidopsis thaliana.

XX WO2004035798-A2.

XX PD 29-APR-2004.

XX PF 20-OCT-2003; 2003WO-EP011658.

XX PR 18-OCT-2002; 2002EP-00079408.

XX (CROP-) CROPDESIGN NV.

XX Inze D, De Veylder L, Vlieghe K;

XX WPI; 2004-348466/32.

XX P-PSDB; ADN74231.

PT Altering plant characteristics, useful for producing plants for enzyme or
pharmaceutical production comprises modifying in a plant, expression of
one or more nucleic acids and/or modifying level or activity of one or
more proteins.

PS Claim 1; SEQ ID NO 2125; 134pp; English.

XX This invention relates to a novel method for altering one or more plant
characteristics. Specifically, it refers to identifying genes that are up
- or down-regulated in transgenic plants overexpressing the heterodimeric

CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
 CC generating plant characteristics accordingly. The present invention describes
 CC generating transgenic plants for the production of growth regulators,
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
 CC the altered plant characteristics are selected from increased yield or
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture
 CC or physiology, altered endoreplication, biochemistry, signal
 CC transduction, storage lipid mobilization and/or altered photosynthesis,
 CC each relative to the corresponding wild type plants. Accordingly, these
 CC sequences can also be useful as positive or negative selectable markers
 CC during transformation of cells or tissues. The identified genes play a
 CC role in a variety of biological processes such as DNA replication, cell
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
 CC transcription factors. This polynucleotide sequence is the E2Fa/Dpa
 CC repressed 1.3 fold or more in plants overexpressing the E2Fa/Dpa
 CC transcription factor, given in an exemplification of the invention.

XX
 SQ Sequence 1617 BP; 389 A; 346 C; 359 G; 523 T; 0 U; 0 Other;

Query Match 74.2%; Score 1617; DB 12; Length 1617;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 ATGTTGGATTCTTAGTCTCGAAGTCCCTTCGTTATCGACATCTGATCAGCTTCTGTG 345
 DB 1 ATGTTGGATTCTTAGTCTCGAAGTCCCTTCGTTATCGACATCTGATCAGCTTCTGTG 60
 QY 346 GTTGGTTGAATCTCTTTGTGACATCTTTGTGCTTGTATCTCTTGTGATCTTTTG 405
 DB 61 GTTGGTTGAATCTCTTTGTGACATCTTTGTGCTTGTATCTCTTGTGATCTTTTG 120
 QY 406 GAAGAGAATAGATGGATGAACGAATCCATCAGCCCTTGTGATTTGGCTAGGCACTGGT 465
 DB 121 GAAGAGAATAGATGGATGAACGAATCCATCAGCCCTTGTGATTTGGCTAGGCACTGGT 180
 QY 466 GTTACCAATTTGTTGATAGTAAGAAAGTTCGCACTTCTCGTCTTTAGTGAAGAT 525
 DB 181 GTTACCAATTTGTTGATAGTAAGAAAGTTCGCACTTCTCGTCTTTAGTGAAGAT 240
 QY 526 CTTTCTTCATATATCTTTTGGCCACCATATATCAATTCAGCGGTTTCAAGTAAAGAAAG 585
 DB 241 CTTTCTTCATATATCTTTTGGCCACCATATATCAATTCAGCGGTTTCAAGTAAAGAAAG 300
 QY 586 AAGCAGTTTTCCGCAATTTCTGACTATTTATGCTTTTGGTCTCTTGGGACTATTTAT 645
 DB 301 AAGCAGTTTTCCGCAATTTCTGACTATTTATGCTTTTGGTCTCTTGGGACTATTTAT 360
 QY 646 TCTTGACATATATCTCTAGTGTAAACAGTTCCTTTAAGAAAGTTGACATTTGAACC 705
 DB 361 TCTTGACATATATCTCTAGTGTAAACAGTTCCTTTAAGAAAGTTGACATTTGAACC 420
 QY 706 TTTGACTTTGGGTGATTATCTTGCTATTTGGTGCATATTTGCTGCAACAGATTTCAGTATGT 765
 DB 421 TTTGACTTTGGGTGATTATCTTGCTATTTGGTGCATATTTGCTGCAACAGATTTCAGTATGT 480
 QY 766 ACACTCAGGTCTCGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTCGAGAG 825
 DB 481 ACACTCAGGTCTCGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTCGAGAG 540
 QY 826 GGTGTTGCAATGATCAAGTTCAGTTGTTGCTTCAACCGGATTCAGAGCTTTGATCTC 885
 DB 541 GGTGTTGCAATGATCAAGTTCAGTTGTTGCTTCAACCGGATTCAGAGCTTTGATCTC 600
 QY 886 ACTCAGCTAAACCAAGCTGCTTTTCTTCTTGGAAACTTCTTGTATTTGTTTCTC 945
 DB 601 ACTCAGCTAAACCAAGCTGCTTTTCTTCTTGGAAACTTCTTGTATTTGTTTCTC 660
 QY 946 CTAAGTACCTTGTGGTGTGCAACCGGTCTGATAGTGCATGTTATCAAGAAGCTA 1005
 DB 661 CTAAGTACCTTGTGGTGTGCAACCGGTCTGATAGTGCATGTTATCAAGAAGCTA 720
 QY 1006 TACTTTGGAGGCACTCACTGACGAGAGTTGCCCTTATGCTTATGCTTATGCGGTATCTT 1065

DB 721 TACTTTGGAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTATGGCGTATCTT 780
 QY 1066 TCTTATATCTTCTGCTGAGCTTTTCCAGCTTGAGCGGTATCCTCACTGTGTTTCTGTGGT 1125
 DB 781 TCTTATATCTTCTGCTGAGCTTTTCCAGCTTGAGCGGTATCCTCACTGTGTTTCTGTGGT 840
 QY 1126 ATTGTGATGTCCTCAATTTACACATGGGCAATGTAACGGAGAGCTCAAGATAACAAAG 1185
 DB 841 ATTGTGATGTCCTCAATTTACACATGGGCAATGTAACGGAGAGCTCAAGATAACAAAG 900
 QY 1186 CATACCTTTGCAACTTTTGTCTTCTTGGGAGACATTTATTTCTTGTATGTTGAATG 1245
 DB 901 CATACCTTTGCAACTTTTGTCTTCTTGGGAGACATTTATTTCTTGTATGTTGAATG 960
 QY 1246 GATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACCGGGAACATCGATCGCA 1305
 DB 961 GATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACCGGGAACATCGATCGCA 1020
 QY 1306 GTGAGCTCAATCTTAATGGGCTCTGGTCTATGGTTGGAAGAGCAGCGTTCTTTCCGTTA 1365
 DB 1021 GTGAGCTCAATCTTAATGGGCTCTGGTCTATGGTTGGAAGAGCAGCGTTCTTTCCGTTA 1080
 QY 1366 TCGTTTCTATCTAACTTAGCCAAAGAAAGTAACAAAGGAGAAATCACTTTTAAATGAG 1425
 DB 1081 TCGTTTCTATCTAACTTAGCCAAAGAAAGTAACAAAGGAGAAATCACTTTTAAATGAG 1140
 QY 1426 GTTGTGATTTGGTGTCTGCTCATGAGAGTCTGTATCTATGCTCTTGCATACAAAC 1485
 DB 1141 GTTGTGATTTGGTGTCTGCTCATGAGAGTCTGTATCTATGCTCTTGCATACAAAC 1200
 QY 1486 AAGTTTACAAGGGCCGGGCACACAGATGTACCGGGAATGCAATCATGATCAGAGTACG 1545
 DB 1201 AAGTTTACAAGGGCCGGGCACACAGATGTACCGGGAATGCAATCATGATCAGAGTACG 1260
 QY 1546 ATAACTGTCTGTCTTTTAGCAGCAGTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1605
 DB 1261 ATAACTGTCTGTCTTTTAGCAGCAGTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1320
 QY 1606 TACCTATTACCGCACACAGAAACCGCACAGATGTATCTGATGACAAACCCCAAA 1665
 DB 1321 TACCTATTACCGCACACAGAAACCGCACAGATGTATCTGATGACAAACCCCAAA 1380
 QY 1666 TCCATACATATCCCTTTTGTGGACCAAGACTCGTTTCTTGTAGGCTTTCAGGGAAACCAAT 1725
 DB 1381 TCCATACATATCCCTTTTGTGGACCAAGACTCGTTTCTTGTAGGCTTTCAGGGAAACCAAT 1440
 QY 1726 GTGCTCTCGGCTGACAGTATAGTGGCTTCTTGACACCGGCCACTCGAAACCGTGCATTAC 1785
 DB 1441 GTGCTCTCGGCTGACAGTATAGTGGCTTCTTGACACCGGCCACTCGAAACCGTGCATTAC 1500
 QY 1786 TACTGGAGACAATTTGATGACTCTCTTCAATGCGACCGCTTTTGGAGGTCGTGGCTTTGTA 1845
 DB 1501 TACTGGAGACAATTTGATGACTCTCTTCAATGCGACCGCTTTTGGAGGTCGTGGCTTTGTA 1560
 QY 1846 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCTGATCTTTAGTAAGGCTTTGA 1902
 DB 1561 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCTGATCTTTAGTAAGGCTTTGA 1617

RESULT 5

ADN11979

ID ADN11979 standard; DNA; 1614 BP.

XX

AC ADN11979;

XX

DT 17-JUN-2004 (first entry)

XX

DE Wild type AtNHX1 encoding sequence.

XX

KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.

XX

OS Arabidopsis thaliana.

XX

| | | |
|----|---|--|
| PH | Key | Location/Qualifiers |
| FT | CDS | 1..1614 |
| FT | | /*tag= a |
| FT | | /product= "AtNHX1" |
| XX | | |
| XX | WO2004007668-A2. | |
| XX | | |
| XX | 22-JAN-2004. | |
| XX | | |
| XX | 09-JUL-2003; 2003WO-US021549. | |
| XX | | |
| XX | 12-JUL-2002; 2002US-0395662P. | |
| XX | | |
| XX | (REGC) UNIV CALIFORNIA. | |
| PA | | |
| XX | Shi H, Blumwald B; | |
| XX | | |
| XX | WPI; 2004-122911/12. | |
| DR | P-PSDB; ADN11980. | |
| DR | | |
| XX | Enhancing salt tolerance of a plant comprises introducing into the plant | |
| PT | a polynucleotide encoding a Na+/H+ transporter polypeptide. | |
| PT | | |
| XX | | |
| XX | Disclosure; SEQ ID NO 1; 38pp; English. | |
| PS | | |
| XX | | |
| CC | The present invention relates to enhancing salt tolerance of a plant | |
| CC | comprises introducing into the plant a polynucleotide encoding a Na+/H+ | |
| CC | transporter polypeptide. The AtNHX1 gene confers salt tolerance. The | |
| CC | composition and methods are useful in conferring salt tolerance on plants | |
| CC | and other organisms. The present sequence represents wild type AtNHX1 | |
| CC | encoding sequence. | |
| XX | | |
| SQ | Sequence 1614 BP; 388 A; 346 C; 358 G; 522 T; 0 U; 0 Other; | |
| | Query Match | 74.1%; Score 1614; DB 12; Length 1614; |
| | Best Local Similarity | 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; |
| | Matches 1614; Conservative | 0; |
| Qy | 286 | ATGTTGGATTCTCTAGTGTGAACTGCGCTTCGTTATCGACATCTGATCAGCGTCTCTGTG 345 |
| Db | 1 | ATGTTGGATTCTCTAGTGTGAACTGCGCTTCGTTATCGACATCTGATCAGCGTCTCTGTG 60 |
| Qy | 346 | GTTCGGTGAATCTCTTTGTGACATCTTTGTGCTGTTGATGTTCTTGGTCAATCTTTTG 405 |
| Db | 61 | GTTCGGTGAATCTCTTTGTGACATCTTTGTGCTGTTGATGTTCTTGGTCAATCTTTTG 120 |
| Qy | 406 | GAAGAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 465 |
| Db | 121 | GAAGAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180 |
| Qy | 466 | GTTACCAATTTGTTGATTAGTAAAGGAAAGCTCGCATCTTCTCGTCTTTTAGTGAAGAT 525 |
| Db | 181 | GTTACCAATTTGTTGATTAGTAAAGGAAAGCTCGCATCTTCTCGTCTTTTAGTGAAGAT 240 |
| Qy | 526 | CTTTTCTCATATATCTTTTGGCACCCATATATCAATGCGAGGTTTCAAGTAAAGAAAG 585 |
| Db | 241 | CTTTTCTCATATATCTTTTGGCACCCATATATCAATGCGAGGTTTCAAGTAAAGAAAG 300 |
| Qy | 586 | AAGCAGTTTTTCGGCAATTTCTGACTATATGCTTTTGGTCTGTTGGGACTATATT 645 |
| Db | 301 | AAGCAGTTTTTCGGCAATTTCTGACTATATGCTTTTGGTCTGTTGGGACTATATT 360 |
| Qy | 646 | TCTTGCAATATATCTCTAGTGTGAACACAGTCTCTTTAAGAAAGTTGGACATTTGAACC 705 |
| Db | 361 | TCTTGCAATATATCTCTAGTGTGAACACAGTCTCTTTAAGAAAGTTGGACATTTGAACC 420 |
| Qy | 706 | TTTGACTTGGGTGATPATCTTCTGATTTGGTGCATATTTGCTGCAACAGATTCAGTATGT 765 |
| Db | 421 | TTTGACTTGGGTGATPATCTTCTGATTTGGTGCATATTTGCTGCAACAGATTCAGTATGT 480 |
| Qy | 766 | ACACTGCAGTCTTGATCAAGACGACACCTTTGCTTTACAGTCTTGTATTCGAGAG 825 |
| Db | 481 | ACACTGCAGTCTTGATCAAGACGACACCTTTGCTTTTACAGTCTTGTATTCGAGAG 540 |

| | | |
|----|------|--|
| Qy | 826 | GGTGTGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATC 885 |
| Db | 541 | GGTGTGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATC 600 |
| Qy | 886 | ACTCAGCTAAACCAAGAGCTGCTTTTCACTCTCTTGGAAACTCTCTGTATTTGTTTCTC 945 |
| Db | 601 | ACTCAGCTAAACCAAGAGCTGCTTTTCACTCTCTTGGAAACTCTCTGTATTTGTTTCTC 660 |
| Qy | 946 | CTAAGTACCTTGGTGGTCTGCAACCGCTCTGATAAGTGGCGTATGTTATCAAGAAAGCTA 1005 |
| Db | 661 | CTAAGTACCTTGGTGGTCTGCAACCGCTCTGATAAGTGGCGTATGTTATCAAGAAAGCTA 720 |
| Qy | 1006 | TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATCTTATGGCGTATCTT 1065 |
| Db | 721 | TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATCTTATGGCGTATCTT 780 |
| Qy | 1066 | TCTTATATGCTTGGTGGTCTTTCGACTTGGGGTATCTCTCACTGTGTTTCTCTGTTG 1125 |
| Db | 781 | TCTTATATGCTTGGTGGTCTTTCGACTTGGGGTATCTCTCACTGTGTTTCTCTGTTG 840 |
| Qy | 1126 | ATTGTGATGTCCTCATTTACATGCGGCAATGTAAACGAGAGCTCAAGAATAACAACAAAG 1185 |
| Db | 841 | ATTGTGATGTCCTCATTTACATGCGGCAATGTAAACGAGAGCTCAAGAATAACAACAAAG 900 |
| Qy | 1186 | CATACCTTTGCAACTTTGTTCATTTCTTCGGGAGACATTTATTTTGTATGTTGGAATG 1245 |
| Db | 901 | CATACCTTTGCAACTTTGTTCATTTCTTCGGGAGACATTTATTTTGTATGTTGGAATG 960 |
| Qy | 1246 | GATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305 |
| Db | 961 | GATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020 |
| Qy | 1306 | GTGAGCTCAATCTTAATGGTCTGTGTCATGTTTGGAAAGAGCAGCGTTCGTCTTTCGGTTA 1365 |
| Db | 1021 | GTGAGCTCAATCTTAATGGTCTGTGTCATGTTTGGAAAGAGCAGCGTTCGTCTTTCGGTTA 1080 |
| Qy | 1366 | TCGTTTCTATCTTAACCTTAGCCAAAGAAATCAAAGCGAGAAATCAACTTTTAACTGCAG 1425 |
| Db | 1081 | TCGTTTCTATCTTAACCTTAGCCAAAGAAATCAAAGCGAGAAATCAACTTTTAACTGCAG 1140 |
| Qy | 1426 | GTTGTGATTTGGTGGTCTCTCATGAGAGTGTGTTATCTATGCTCTTGTGATACAC 1485 |
| Db | 1141 | GTTGTGATTTGGTGGTCTCTCATGAGAGTGTGTTATCTATGCTCTTGTGATACAC 1200 |
| Qy | 1486 | AAGTTTACAAAGCGCGGCGACACAGATGTACCGGGAATGCAATCATGATCAGAGTACG 1545 |
| Db | 1201 | AAGTTTACAAAGCGCGGCGACACAGATGTACCGGGAATGCAATCATGATCAGAGTACG 1260 |
| Qy | 1546 | ATAACTGTCTGTCTTTTATAGCAAGTGTGTTTGGTATGCTGACCAAAACCACTCATAAGC 1605 |
| Db | 1261 | ATAACTGTCTGTCTTTTATAGCAAGTGTGTTTGGTATGCTGACCAAAACCACTCATAAGC 1320 |
| Qy | 1606 | TACCTATTACCGCACGAGAACCGCACAGAGATGTTATCTGATGACAAACACCCCAAA 1665 |
| Db | 1321 | TACCTATTACCGCACGAGAACCGCACAGAGATGTTATCTGATGACAAACACCCCAAA 1380 |
| Qy | 1666 | TCATACATATCTCTTTTGGACCAAGACTCGTTTCAATGAGCTTTCAGGGAACCAAT 1725 |
| Db | 1381 | TCATACATATCTCTTTTGGACCAAGACTCGTTTCAATGAGCTTTCAGGGAACCAAT 1440 |
| Qy | 1726 | GTGCTCTCGGCTTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1785 |
| Db | 1441 | GTGCTCTCGGCTTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500 |
| Qy | 1786 | TAAGTGGAGCAATTTGATGATCTCTTCATGCAACCGCTCTTTGGAGGTCTGGCTTTGTA 1845 |
| Db | 1501 | TAAGTGGAGCAATTTGATGATCTCTTCATGCAACCGCTCTTTGGAGGTCTGGCTTTGTA 1560 |
| Qy | 1846 | CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAGGCT 1899 |
| Db | 1561 | CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAGGCT 1614 |

| Query Match | Best Local Similarity | Score | 1612.4; | DB 12; | Length 1614; |
|---------------|---|---------------|-----------|---------|--------------|
| Matches 1613; | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; | |
| 286 | ATGTGATCTCTAGTTCGAACTCGCTTCGTTATCGACATCTGATCGATCGCTTCGTG | 345 | | | |
| 1 | ATGTGGATCTCTAGTTCGAACTCGCTTCGTTATCGACATCTGATCGATCGCTTCGTG | 60 | | | |
| 346 | GTTCGCTGAATCTCTTTGTCACCTCTTTGCTGCTTGTATGTTCTTTGGTCACTTTTG | 405 | | | |
| 61 | GTTCGCTGAATCTCTTTGTCACCTCTTTGCTGCTTGTATGTTCTTTGGTCACTTTTG | 120 | | | |
| 406 | GAGAGAAATAGATGGAATGAACGAATCCATCCGCTTTGTTGATTTGGCTAGGCACTGGT | 465 | | | |
| 121 | GAGAGAAATAGATGGAATGAACGAATCCATCCGCTTTGTTGATTTGGCTAGGCACTGGT | 180 | | | |
| 466 | GTTCACATTTTGTGTTAGTAAAGGAAAGCTCGCATCTCTCGTCTTTAGTGAAGAT | 525 | | | |
| 181 | GTTCACATTTTGTGTTAGTAAAGGAAAGCTCGCATCTCTCGTCTTTAGTGAAGAT | 240 | | | |
| 526 | CTTTTCTTCATATATCTTTTGGCCACCAATATATATCAATGACGGTTTCAAGTAAAAAG | 585 | | | |
| 241 | CTTTTCTTCATATATCTTTTGGCCACCAATATATATCAATGACGGTTTCAAGTAAAAAG | 300 | | | |
| 586 | AAGCAGTTTTCCGCAATTTCTGAGACTATATGCTTTTGGTCTGTTGGCACTATTAT | 645 | | | |
| 301 | AAGCAGTTTTCCGCAATTTCTGAGACTATATGCTTTTGGTCTGTTGGCACTATTAT | 360 | | | |
| 646 | TCCTGCACAAATCATATCTCTAGTGTGAACACAGATTTCTTTAAGAAAGTTGGACATTTGGAACC | 705 | | | |

Db 1441 GTGCCTGGCTGACAGTATACGTGGCTTCTTGACAGCGCCACTCGAACCGTGCAATTAC 1500
Qy 1786 TACTGGAGACAATTTGATGACTCCTTCATCGCACCGCTCTTTGGAGGTGCTGGCTTTGTA 1845
Db 1501 TACTGGAGACAATTTGATGACTGCTTCATCGCACCGCTCTTTGGAGGTGCTGGCTTTGTA 1560
Qy 1846 CCGTTTGTCCAGGTTCTCAACTGAGAGAAACCCCTCCTGATCTTAGTAAGGCT 1899
Db 1561 CCGTTTGTCCAGGTTCTCAACTGAGAGAAACCCCTCCTGATCTTAGTAAGGCT 1614

RESULT 7
ADN11983
ID ADN11983 standard; DNA; 1563 BP.
XX AC
XX ADN11983;
XX 17-JUN-2004 (first entry)
DT ATNHX1 mutant encoding sequence #2.
XX salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.
XX Synthetic.
XX WO2004007668-A2.
XX PN 22-JAN-2004.
XX 09-JUL-2003; 2003WO-US021549.
XX PR 12-JUL-2002; 2002US-0395662P.
XX (REGC) UNIV CALIFORNIA.
XX PA Shi H, Blumwald B;
XX PI WPI; 2004-122911/12.
XX DR P-PSDB; ADN11984.
XX DR Enhancing salt tolerance of a plant comprises introducing into the plant
PT a polynucleotide encoding a Na+/H+ transporter polypeptide.
XX Claim 2; SEQ ID NO 5; 38pp; English.
XX The present invention relates to enhancing salt tolerance of a plant
CC comprises introducing into the plant a polynucleotide encoding a Na+/H+
CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The
CC composition and methods are useful in conferring salt tolerance on plants
CC and other organisms. The present sequence represents a mutant AtNHX1
CC encoding sequence.
XX Sequence 1563 BP; 376 A; 333 C; 348 G; 506 T; 0 U; 0 Other;
SQ

Query Match 71.8%; Score 1563; DB 12; Length 1563;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 286 ATGTGGATCTCTAGTGTGGAACCTCGCTTATCGACATCTGATCAGCGTTCTGTG 345
Db 1 ATGTTGGATTCTCTAGTGTGGAACCTCGCTTATCGACATCTGATCAGCGTTCTGTG 60
Qy 346 GTTGGCTTGAATCTCTTTGTGACATCTTTGTGCTTGTATTCTTTGCTCATCTTTTG 405
Db 61 GTTGGCTTGAATCTCTTTGTGACATCTTTGTGCTTGTATTCTTTGCTCATCTTTTG 120
Qy 406 GAAGAGATAGATGGATGAACGAATCCATCAGCGCTTGTGATTTGGGCTAGGCACTGGT 465
Db 121 GAAGAGATAGATGGATGAACGAATCCATCAGCGCTTGTGATTTGGGCTAGGCACTGGT 180
Qy 466 GTTACCATTTTGTGATTTAGTAAGGAAAGTTCGCACTCTTCTGCTTTTAGTGAAGAT 525
Db 181 GTTACCATTTTGTGATTTAGTAAGGAAAGTTCGCACTCTTCTGCTTTTAGTGAAGAT 240

Qy 526 CTTTCTTCATATATCTTTTGGCCACCCATATATTAATCAATGACGGGTTTCAAGTAAAAAG 585
Db 241 CTTTCTTCATATATCTTTTGGCCACCCATATATTAATCAATGACGGGTTTCAAGTAAAAAG 300
Qy 586 AAGCAGTTTTCGCGCAATTTTCTGCTGACTATTAATGCTTTTGGTGTCTGCTGGACTATTATT 645
Db 301 AAGCAGTTTTCGCGCAATTTTCTGCTGACTATTAATGCTTTTGGTGTCTGCTGGACTATTATT 360
Qy 646 TCTTGCAATCATATCTCTAGGTGTAAACAAGTCTCTTTAAGAAAGTTGACATTTGGAACC 705
Db 361 TCTTGCAATCATATCTCTAGGTGTAAACAAGTCTCTTTAAGAAAGTTGACATTTGGAACC 420
Qy 706 TTTGACTTGGGTGATTAATCTTGTCTATTTGTCATATTTGTCGCAATTTGTCGCAATTCAGTATGT 765
Db 421 TTTGACTTGGGTGATTAATCTTGTCTATTTGTCATATTTGTCGCAATTTGTCGCAATTCAGTATGT 480
Qy 766 AACTGCAAGTTCTGAAATCAAGACGAGACACCTTTGCTTTTACAGTCTTCTATTTCGAGAG 825
Db 481 AACTGCAAGTTCTGAAATCAAGACGAGACACCTTTGCTTTTACAGTCTTCTATTTCGAGAG 540
Qy 826 CGTGTGTGAATGATGCAACAGTCAAGTGTGGTCTTCAACGCGATTTCAGAGCTTTGATCTC 885
Db 541 GGTGTGTGAATGATGCAACAGTCAAGTGTGGTCTTCAACGCGATTTCAGAGCTTTGATCTC 600
Qy 886 ACTCACCTAAACCCAGAAAGCTGCTTTTCAATCTTCTTGGAACTTCTTGTATTGTTTCTC 945
Db 601 ACTCACCTAAACCCAGAAAGCTGCTTTTCAATCTTCTTGGAACTTCTTGTATTGTTTCTC 660
Qy 946 CTAAGTACCTTCTGCTGGTGTCTCAACCGCTCTGATTAAGTGCCTTATTAAGAGCTTA 1005
Db 661 CTAAGTACCTTCTGCTGGTGTCTCAACCGCTCTGATTAAGTGCCTTATTAAGAGAGCTTA 720
Qy 1006 TACTTTGGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATGCTTATGGCTATCTT 1065
Db 721 TACTTTGGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATGCTTATGGCTATCTT 780
Qy 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTGAGCGGTATCCTCACTGTGTTTTCTGTGTT 1125
Db 781 TCTTATATGCTTGTGAGCTTTTTCGACTTGAGCGGTATCCTCACTGTGTTTTCTGTGTT 840
Qy 1126 ATGTGATGTCCTCATTAACATGACATGCAATGTAACGAGAGCTCAAGATTAACAACAAAG 1185
Db 841 ATGTGATGTCCTCATTAACATGACATGCAATGTAACGAGAGCTCAAGATTAACAACAAAG 900
Qy 1186 CATACCTTTGCAACTTTTGTCACTTTCTGCGAGACATTTATTTTCTTGTATGTTGGAATG 1245
Db 901 CATACCTTTGCAACTTTTGTCACTTTCTGCGAGACATTTATTTTCTTGTATGTTGGAATG 960
Qy 1246 GATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305
Db 961 GATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020
Qy 1306 GTGAGCTCAATCCTTAATGSGTCTGCTCATGTTTGGAGAGCAGCTTCTGCTTTCCGTTA 1365
Db 1021 GTGAGCTCAATCCTTAATGSGTCTGCTCATGTTTGGAGAGCAGCTTCTGCTTTCCGTTA 1080
Qy 1366 TCGTTTCTATCTAACTTAGCCAAGAGAAATCAAGCGAGAAATCAACTTTTAACATGCGAG 1425
Db 1081 TCGTTTCTATCTAACTTAGCCAAGAGAAATCAAGCGAGAAATCAACTTTTAACATGCGAG 1140
Qy 1426 GTTGTGATTTGGTGTGCTGCTCATGAGAGGTGCTGTATCTATGAGTCTTGTGATCAAC 1485
Db 1141 GTTGTGATTTGGTGTGCTGCTCATGAGAGGTGCTGTATCTATGAGTCTTGTGATCAAC 1200
Qy 1486 AAGTTTAAAGGGCGGGGCAACAGATGACGCGGGAATGCAATCATGATCAGAGTACG 1545
Db 1201 AAGTTTAAAGGGCGGGGCAACAGATGACGCGGGAATGCAATCATGATCAGAGTACG 1260
Qy 1546 ATAACTGCTGCTCTTTTGTAGCACAGTGGTGTGTTGATGCTGACCAAAACCACTCATAAGC 1605
Db 1261 ATAACTGCTGCTCTTTTGTAGCACAGTGGTGTGTTGATGCTGACCAAAACCACTCATAAGC 1320

QY 1606 TACATATTACCGCACCGAACGCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1665
 Db 1321 TACATATTACCGCACCGAACGCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1380
 QY 1666 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTTCAATGAGCCTTCAGGAAACCAAT 1725
 Db 1381 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTTCAATGAGCCTTCAGGAAACCAAT 1440
 QY 1726 GTGCTCGGCTGACAGTATAGTGGCTTCTTGACACGGCCCACTCGAACCGTGCATTAC 1785
 Db 1441 GTGCTCGGCTGACAGTATAGTGGCTTCTTGACACGGCCCACTCGAACCGTGCATTAC 1500
 QY 1786 TACTGGAGACAATTTGATGACTCCTTCATCGACCCCGTCTTTGGAGTCTGTGGCTTTGTA 1845
 Db 1501 TACTGGAGACAATTTGATGACTCCTTCATCGACCCCGTCTTTGGAGTCTGTGGCTTTGTA 1560
 QY 1846 CCC 1848
 Db 1561 CCC 1563

RESULT 8
 ADN11989
 ID ADN11989 standard; cDNA; 1566 BP.
 XX AC ADN11989;
 XX DT 17-JUN-2004 (first entry)
 XX DE NDL-1 encoding sequence.
 XX KW salt tolerance; Na⁺/H⁺ transporter polypeptide; AtNHX1; ss.
 XX OS Saccharomyces sp.
 XX PN WO2004007668-A2.
 XX PD 22-JAN-2004.
 XX PF 09-JUL-2003; 2003WO-US021549.
 XX PR 12-JUL-2002; 2002US-0395662P.
 XX PS (REGC) UNIV CALIFORNIA.
 XX PI Shi H, Blumwald E;
 XX DR WPI; 2004-122911/12.
 XX DR P-PSDB; ADN11990.
 PT Enhancing salt tolerance of a plant comprises introducing into the plant
 PT a polynucleotide encoding a Na⁺/H⁺ transporter polypeptide.
 XX Claim 2; SEQ ID NO 11; 38pp; English.
 CC The present invention relates to enhancing salt tolerance of a plant
 CC comprises introducing into the plant a polynucleotide encoding a Na⁺/H⁺
 CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The
 CC composition and methods are useful in conferring salt tolerance on plants
 CC and other organisms. The present sequence represents NDL-1 encoding
 CC sequence.
 XX Sequence 1566 BP; 378 A; 334 C; 349 G; 505 T; 0 U; 0 Other;
 SQ

Query Match 71.8%; Score 1563; DB 12; Length 1566;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 337 GCTTCGTGGTGGTGAATCTCTTTGTTGCACTTCTTTGTCCTTGATGTTCTTGGT 396
 Db 4 GCTTCGTGGTGGTGAATCTCTTTGTTGCACTTCTTTGTCCTTGATGTTCTTGGT 63
 QY 397 CATCTTTTGGAGAGATAGATGGATGAACCAATCCATCACCCTTGTGATGGGCTA 456

Db 64 CATCTTTTGGAGAGATAGATGGATGAACCAATCCATCACCCTTGTGATGGGCTA 123
 QY 457 GGCACGTGGTGTACCATTTTGTGTAGTAAGAGAAAAGCTCGCATCTTCTGCTTTT 516
 Db 124 GGCACGTGGTGTACCATTTTGTGTAGTAAGAGAAAAGCTCGCATCTTCTGCTTTT 183
 QY 517 AGTGAAGATCTTTTCTTCATATATCTTTTGGCCACCATATATTCATCGAGGTTTCAA 576
 Db 184 AGTGAAGATCTTTTCTTCATATATCTTTTGGCCACCATATATTCATCGAGGTTTCAA 243
 QY 577 GTAAAAAAGAGCAGTTTTTTCGCAATTTTCGTGACTATTTATGCTTTTGGTGTGTTGG 636
 Db 244 GTAAAAAAGAGCAGTTTTTTCGCAATTTTCGTGACTATTTATGCTTTTGGTGTGTTGG 303
 QY 637 ACTATATTTTCTTGCAATCATATCTCTAGGTGTAAACAGTTCTTTAAGAGTTGGAC 696
 Db 304 ACTATATTTTCTTGCAATCATATCTCTAGGTGTAAACAGTTCTTTAAGAGTTGGAC 363
 QY 697 ATTGGAACCTTTGACTTGGGTGATTATCTTGCTATTGTGGCCATATTTCTGTCACAGAT 756
 Db 364 ATTGGAACCTTTGACTTGGGTGATTATCTTGCTATTGTGGCCATATTTCTGTCACAGAT 423
 QY 757 TCAGTATGTACACTCGAGTTCTGAAATCAAGACGAGACACCTTTGCTTTACAGTCTTGT 816
 Db 424 TCAGTATGTACACTCGAGTTCTGAAATCAAGACGAGACACCTTTGCTTTACAGTCTTGT 483
 QY 817 TTGGAGAGGGTGTGTGAAATGATCAAGCTCAGTTGTGCTTCAACGCGATTACAGAC 876
 Db 484 TTGGAGAGGGTGTGTGAAATGATCAAGCTCAGTTGTGCTTCAACGCGATTACAGAC 543
 QY 877 TTTGATCTCACTCACTAAACCAAGCTGCTTTTTCATCTTCTTGGAACTTCTTGAT 936
 Db 544 TTTGATCTCACTCACTAAACCAAGCTGCTTTTTCATCTTCTTGGAACTTCTTGAT 603
 QY 937 TTGTTTCTCTAAGTACCTTGTGCTGCTCAACCGGTCTGATAAGTGCCTGATGTTATC 996
 Db 604 TTGTTTCTCTAAGTACCTTGTGCTGCTCAACCGGTCTGATAAGTGCCTGATGTTATC 663
 QY 997 AAGAGCTATATCTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTATG 1056
 Db 664 AAGAGCTATATCTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTATG 723
 QY 1057 GCGTATCTTTCTTATATGCTTGTGCTGCTTTTCGACTTTGAGCGGTATCTCACTGTGTT 1116
 Db 724 GCGTATCTTTCTTATATGCTTGTGCTGCTTTTCGACTTTGAGCGGTATCTCACTGTGTT 783
 QY 1117 TTCTGTGTATTTGTGATGTCCCATTTACATGGCACAATGTAAACGAGAGCTCAAGAATA 1176
 Db 784 TTCTGTGTATTTGTGATGTCCCATTTACATGGCACAATGTAAACGAGAGCTCAAGAATA 843
 QY 1177 ACAACAAAGCATACCTTTTGGCAACTTTTGTCACTTTTGGCGAGACATTTATTTCTTGTT 1236
 Db 844 ACAACAAAGCATACCTTTTGGCAACTTTTGTCACTTTTGGCGAGACATTTATTTCTTGTT 903
 QY 1237 GTTGAATGGATGCTTTCGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACA 1296
 Db 904 GTTGAATGGATGCTTTCGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACA 963
 QY 1297 TCGATCGAGTGAGTCAATCCTTAATGGTCTGTGCTGTTGTTGGAAGAGCGGTTGCTG 1356
 Db 964 TCGATCGAGTGAGTCAATCCTTAATGGTCTGTGCTCATGTTGGAAGAGCGGTTGCTG 1023
 QY 1357 TTTCCGTTATCGTTTCTATCTAACTTAGCCAAAGAAATCAAGCGGAGAAATCAACTTTT 1416
 Db 1024 TTTCCGTTATCGTTTCTATCTAACTTAGCCAAAGAAATCAAGCGGAGAAATCAACTTTT 1083
 QY 1417 AACATGCAAGTGTGATTTGGTGTGCTGCTCATGAGAGGTGCTGTATCTATGCTCTT 1476
 Db 1084 AACATGCAAGTGTGATTTGGTGTGCTGCTCATGAGAGGTGCTGTATCTATGCTCTT 1143
 QY 1477 GCATACACAGTTTACAAAGGCGGCGGACACAGATGTACGGGGAGTGCATCATGATC 1536

Db 1144 GCATACAAAGTTTACAGGGCGGGGCACACAGATGTAGCGGGGAATGCAATCATGATC 1203
QY 1537 ACAGTACGATAAAGTCTGTCTCTTTTGTAGCACAGTGGTGTGGTATGCTGACCAACCA 1596
Db 1204 ACAGTACGATAAAGTCTGTCTCTTTTGTAGCACAGTGGTGTGGTATGCTGACCAACCA 1263
QY 1597 CTATAGCTACCTATTACCGGACCGAGACCGACCGACCGACCGACCGACCGACCGACCG 1656
Db 1264 CTATAGCTACCTATTACCGGACCGAGACCGACCGACCGACCGACCGACCGACCGACCG 1323
QY 1657 ACCCAAAATCCATACATATCCCTTTGTTGGACCAAGACTCGTTTATTGAGCCCTTCAGGG 1716
Db 1324 ACCCAAAATCCATACATATCCCTTTGTTGGACCAAGACTCGTTTATTGAGCCCTTCAGGG 1383
QY 1717 AACCAAAATGTCCTCGGCTGACAGTATACGTTGCTTCTTGACAGCGCCCACTCGAACC 1776
Db 1384 AACCAAAATGTCCTCGGCTGACAGTATACGTTGCTTCTTGACAGCGCCCACTCGAACC 1443
QY 1777 GTGCATTACTAGGAGACAAATTTGATGACTCTTTCATGGACCGCTTTGGAGTCTGT 1836
Db 1444 GTGCATTACTAGGAGACAAATTTGATGACTCTTTCATGGACCGCTTTGGAGTCTGT 1503
QY 1837 GGTCTTTGTACCCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAG 1896
Db 1504 GGTCTTTGTACCCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAG 1563
QY 1897 GCT 1899
Db 1564 GCT 1566

RESULT 9

ADN11985

ID ADN11985 standard; DNA; 1473 BP.

XX AC

XX ADN11985;

XX DT

17-JUN-2004 (first entry)

XX DE

AtNHX1 mutant encoding sequence #3.

XX KW

salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.

XX OS

Synthetic.

XX PN

WO2004/007668-A2.

XX PD

22-JAN-2004.

XX PF

09-JUL-2003; 2003WO-US021549.

XX PR

12-JUL-2002; 2002US-0395662P.

XX PA

(REGC) UNIV CALIFORNIA.

XX PI

Shi H, Blumwald E;

XX DR

WPI: 2004-122911/12.

XX DR

P-PSDB; ADN11986.

XX PT

Enhancing salt tolerance of a plant comprises introducing into the plant

XX PS

a polynucleotide encoding a Na+/H+ transporter polypeptide.

XX CC

Claim 4; SEQ ID NO 7; 38pp; English.

XX CC

The present invention relates to enhancing salt tolerance of a plant

XX CC

comprises introducing into the plant a polynucleotide encoding a Na+/H+

XX CC

transporter polypeptide. The AtNHX1 gene confers salt tolerance. The

XX CC

composition and methods are useful in conferring salt tolerance on plants

XX CC

and other organisms. The present sequence represents a mutant AtNHX1

XX SQ

encoding sequence.

Sequence 1473 BP; 358 A; 306 C; 327 G; 482 T; 0 U; 0 Other;

Query Match 67.6%; Score 1473; DB 12; Length 1473;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 ATGTTGGATCTCTAGTGTGGAACCTGCTTATCGACATCTGATCAGCGTTCGTG 345
Db 1 ATGTTGGATCTCTAGTGTGGAACCTGCTTATCGACATCTGATCAGCGTTCGTG 60
QY 346 GTTGCCTTCAATCTCTTTGTTGACATCTTTGTTGCTTGTATGTTCTTGTGCTATCTTTTG 405
Db 61 GTTGCCTTCAATCTCTTTGTTGACATCTTTGTTGCTTGTATGTTCTTGTGCTATCTTTTG 120
QY 406 GAAGAGATAGATGGATGAACGAATCCATCAACGCTTGTGTTGATGGGTAGGACATGTT 465
Db 121 GAAGAGATAGATGGATGAACGAATCCATCAACGCTTGTGTTGATGGGTAGGACATGTT 180
QY 466 GTTACCAATTTCTGATAGTAAAGGAAAGCTCGCATCTCTCTCTTTAGTGAAGAT 525
Db 181 GTTACCAATTTCTGATAGTAAAGGAAAGCTCGCATCTCTCTCTTTAGTGAAGAT 240
QY 526 CTTTCTTTCATATATCTTTTGGCACCCTATATATCAATCGAGGGTTTCAAAGTAAAAAG 585
Db 241 CTTTCTTTCATATATCTTTTGGCACCCTATATATCAATCGAGGGTTTCAAAGTAAAAAG 300
QY 586 AAGCAGTTTTCGCAATTTCTGACTATATATGCTTTTGTGCTGCTGTTGGACTATATT 645
Db 301 AAGCAGTTTTCGCAATTTCTGACTATATATGCTTTTGTGCTGCTGTTGGACTATATT 360
QY 646 TCTTGCACATCATATCTCTAGGTGAACACAGTCTCTTTAAGAGTTGACATTTGGAACC 705
Db 361 TCTTGCACATCATATCTCTAGGTGAACACAGTCTCTTTAAGAGTTGACATTTGGAACC 420
QY 706 TTTGACTTGGGTGATTATCTGCTATTGGTGCCATATTTGCTGCAACAGATTCAGTATGT 765
Db 421 TTTGACTTGGGTGATTATCTGCTATTGGTGCCATATTTGCTGCAACAGATTCAGTATGT 480
QY 766 ACACGTGAGTTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTGAGAG 825
Db 481 ACACGTGAGTTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTGAGAG 540
QY 826 GGTGTTGTAATGATGCAACGTCAGTTGGTGTCTTCAACGCGATTCAGAGCTTTGATCTC 885
Db 541 GGTGTTGTAATGATGCAACGTCAGTTGGTGTCTTCAACGCGATTCAGAGCTTTGATCTC 600
QY 886 ACTCACCTAAACACGAGCTGCTTTTCACTCTTCTGGAAACTTCTGTATTGTTTCTC 945
Db 601 ACTCACCTAAACACGAGCTGCTTTTCACTCTTCTGGAAACTTCTGTATTGTTTCTC 660
QY 946 CTAAGTACCTTGTGTTGCTGCAACCGGTCTGATAAGTCCGCTATGTTATCAAGAGACTA 1005
Db 661 CTAAGTACCTTGTGTTGCTGCAACCGGTCTGATAAGTCCGCTATGTTATCAAGAGACTA 720
QY 1006 TACTTTGGAAGGCACTCAACTGACGAGAGTTGCCCTTATGATGCTTATGGGCTATCTT 1065
Db 721 TACTTTGGAAGGCACTCAACTGACGAGAGTTGCCCTTATGATGCTTATGGGCTATCTT 780
QY 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTCACTGTGTTTCTGTGGT 1125
Db 781 TCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTCACTGTGTTTCTGTGGT 840
QY 1126 ATTGTGATGCCATTTACACATGGCACAATGTAACGAGAGCTTCAAGATAAACAACAAAG 1185
Db 841 ATTGTGATGCCATTTACACATGGCACAATGTAACGAGAGCTTCAAGATAAACAACAAAG 900
QY 1186 CATACCTTTGCAACTTTGTTCATTTCTGGGAGACATTTATTTCTTGTATGTTGAATG 1245
Db 901 CATACCTTTGCAACTTTGTTCATTTCTGGGAGACATTTATTTCTTGTATGTTGAATG 960
QY 1246 GATGCTTGGACATTTGACAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305
Db 961 GATGCTTGGACATTTGACAAGTGGAGATCCGTGAGTGAGTGGAGTCCGTTGAGTGGAGTGGAGTCCGATCGCA 1020

QY 1306 GTGAGCTCAATCTTAAGGGTCTGGTCATGTTGGAGAGCAGGTCCTTCCGTTA 1365
 Db 1021 GTGAGCTCAATCTTAAGGGTCTGGTCATGTTGGAGAGCAGGTCCTTCCGTTA 1080
 QY 1366 TCGTTTCTATCTAATCTTAGCCAGAGAAATCAAGCCGAGAAATCAATCTTAAGCAG 1425
 Db 1081 TCGTTTCTATCTAATCTTAGCCAGAGAAATCAAGCCGAGAAATCAATCTTAAGCAG 1140
 QY 1426 GTTGTGATTTGGTGGTCTCTCATGAGAGGTCCTGTATCTATGCTCTTGGCATAAAC 1485
 Db 1141 GTTGTGATTTGGTGGTCTCTCATGAGAGGTCCTGTATCTATGCTCTTGGCATAAAC 1200
 QY 1486 AAGTTTCAAGGGCCGGGACACAGATGTACCGGGGAATGCAATCATGATCAGAGTACG 1545
 Db 1201 AAGTTTCAAGGGCCGGGACACAGATGTACCGGGGAATGCAATCATGATCAGAGTACG 1260
 QY 1546 ATAATCTGCTCTCTTTTATAGCAGAGTGTGTTGGTATGCTGACCAACCACTCATAGC 1605
 Db 1261 ATAATCTGCTCTCTTTTATAGCAGAGTGTGTTGGTATGCTGACCAACCACTCATAGC 1320
 QY 1606 TACCTATTACCGCACCAAGACCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1665
 Db 1321 TACCTATTACCGCACCAAGACCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1380
 QY 1666 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTTCATTGAGCCTTCAGGGAACCAAT 1725
 Db 1381 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTTCATTGAGCCTTCAGGGAACCAAT 1440
 QY 1726 GTGCTCGGCTGACAGTATACGTGGCTCTTG 1758
 Db 1441 GTGCTCGGCTGACAGTATACGTGGCTCTTG 1473

RESULT 10

ADN11991

ID ADN11991 standard; cDNA; 1410 BP.

XX

AC ADN11991;

XX

DT 17-JUN-2004 (first entry)

XX

DE NDL-2 encoding sequence.

XX

KW salt tolerance; Na⁺/H⁺ transporter polypeptide; AtNHX1; ss.

XX

OS Saccharomyces sp.

XX

PN WO2004007668-A2.

XX

PD 22-JAN-2004.

XX

PF 09-JUL-2003; 2003WO-US021549.

XX

PR 12-JUL-2002; 2002US-0395662P.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Shi H, Blumwald E;

XX

DR WPI; 2004-122911/12.

XX

DR P-PSDB; ADN11992.

XX

PT Enhancing salt tolerance of a plant comprises introducing into the plant

XX

PT a polynucleotide encoding a Na⁺/H⁺ transporter polypeptide.

XX

PS Claim 4; SEQ ID NO 13; 38pp; English.

XX

CC The present invention relates to enhancing salt tolerance of a plant
 CC comprises introducing into the plant a polynucleotide encoding a Na⁺/H⁺
 CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The
 CC composition and methods are useful in conferring salt tolerance on plants
 CC and other organisms. The present sequence represents NDL-2 encoding
 CC sequence.

XX SQ Sequence 1410 BP; 348 A; 309 C; 309 G; 444 T; 0 U; 0 Other;
 Query Match 64.6%; Score 1407; DB 12; Length 1410;
 Best Local Similarity 100.0%; Pred. No. 6.7e-308;
 Matches 1407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 493 AAAAGCTCCGACCTTCTCGTCTTTAGTGAAGATCTTTCTCATATATCTTTGGCCACCC 552
 Db 4 AAAAGCTCCGACCTTCTCGTCTTTAGTGAAGATCTTTCTCATATATCTTTGGCCACCC 63
 QY 553 ATTATATTCAATGACGGGTTTCAAGTAAAGAGAGCAGTTTTTCCGCAATTTCTGACT 612
 Db 64 ATTATATTCAATGACGGGTTTCAAGTAAAGAGAGCAGTTTTTCCGCAATTTCTGACT 123
 QY 613 ATTATGCTTTTGGTGGTCTGTTGGGACTATATTTCTTGACAAATCATATCTCTAGGTGA 672
 Db 124 ATTATGCTTTTGGTGGTCTGTTGGGACTATATTTCTTGACAAATCATATCTCTAGGTGA 183
 QY 673 ACACAGTCTTTTAAAGAGTTGACATTGGAACCTTTGACTTGGGTGATTTCTTGTATT 732
 Db 184 ACACAGTCTTTTAAAGAGTTGACATTGGAACCTTTGACTTGGGTGATTTCTTGTATT 243
 QY 733 GGTGCCATATTTGCTGCAACAGATTCACTGATATGACATGTCAGGTTCTGTAATCAAGACGAG 792
 Db 244 GGTGCCATATTTGCTGCAACAGATTCACTGATATGACATGTCAGGTTCTGTAATCAAGACGAG 303
 QY 793 ACACCTTTTGTCTTACAGTCTTGTATTCGGAGAGGTTGTGAATGATGCAACGTCAGTT 852
 Db 304 ACACCTTTTGTCTTACAGTCTTGTATTCGGAGAGGTTGTGAATGATGCAACGTCAGTT 363
 QY 853 GTGGTCTTCAACGCGATTCAAGAGCTTTGATCTCACTCACTAAACACAGCACTGCTTTT 912
 Db 364 GTGGTCTTCAACGCGATTCAAGAGCTTTGATCTCACTCACTAAACACAGCACTGCTTTT 423
 QY 913 CATCTTTTGGAAACTTCTTGTATTTGTTTCTTAAAGTACCTTCTGTTGGTCTGCAACC 972
 Db 424 CATCTTTTGGAAACTTCTTGTATTTGTTTCTTAAAGTACCTTCTGTTGGTCTGCAACC 483
 QY 973 GGTCTGATAAGTGCGTATGTTATCAAGAGCTATATCTTGGAGGCACTCAACTGACCGA 1032
 Db 484 GGTCTGATAAGTGCGTATGTTATCAAGAGCTATATCTTGGAGGCACTCAACTGACCGA 543
 QY 1033 GAGGTGCCCCCTTATGATGCTTATGGCGTATCTTTCTTATATGCTTGGTCTTTCGAC 1092
 Db 544 GAGGTGCCCCCTTATGATGCTTATGGCGTATCTTTCTTATATGCTTGGTCTTTCGAC 603
 QY 1093 TTGAGCGGTATCCTCACTGTTTCTGTTGTTATGTTGATGTTGCCATTACATGGGCAC 1152
 Db 604 TTGAGCGGTATCCTCACTGTTTCTGTTGTTATGTTGATGTTGCCATTACATGGGCAC 663
 QY 1153 AATGTAAACGAGAGCTCAAGAAATAACAAGAGCATACCTTTGCAACTTTGTCTTCTT 1212
 Db 664 AATGTAAACGAGAGCTCAAGAAATAACAAGAGCATACCTTTGCAACTTTGTCTTCTT 723
 QY 1213 GCGGAGACATTTATTTTCTTGTATGTTGGAATGGAATGCTTTGGACATTTGACAAGTGGAGA 1272
 Db 724 GCGGAGACATTTATTTTCTTGTATGTTGGAATGGAATGCTTTGGACATTTGACAAGTGGAGA 783
 QY 1273 TCCGTGAGTGACACACCGGGAACATCGATCGAGTGAGCTCAATCTTAATGGTCTGGTC 1332
 Db 784 TCCGTGAGTGACACACCGGGAACATCGATCGAGTGAGCTCAATCTTAATGGTCTGGTC 843
 QY 1333 ATGGTTGGAAGAGCAGCGTTCTGTTCCGTTATCGTTTCTTCTTCTTCTTCTTCTTCTT 1392
 Db 844 ATGGTTGGAAGAGCAGCGTTCTGTTCCGTTATCGTTTCTTCTTCTTCTTCTTCTTCTT 903
 QY 1393 AATCAAGCGAGAAATCAACTTTAAACATGAGGTTGATTTGGTGGTCTGGTCTCATG 1452
 Db 904 AATCAAGCGAGAAATCAACTTTAAACATGAGGTTGATTTGGTGGTCTGGTCTCATG 963
 QY 1453 AGAGTGTCTGATCTATGAGTCTTGGCATAACAAGTTTCAAGGGCGGCGGACACAT 1512

Db 964 AGAGTGCTGATCTATGCTTGTGCATACAAACAGTTTACAGGGCGGGCACACAGAT 1023
Qy 1513 GTACGGGGAAATCAATCATGATCAGAGTACGATAACTGCTGTCTTTTACACAGTG 1572
Db 1024 GTACGGGGAAATCAATCATGATCAGAGTACGATAACTGCTGTCTTTTACACAGTG 1083
Qy 1573 GTCTTTGGTATGCTGACCAACACATCAATAGCTTACCTATTACGGACACAGAGCCACC 1632
Db 1084 GTCTTTGGTATGCTGACCAACACATCAATAGCTTACCTATTACGGACACAGAGCCACC 1143
Qy 1633 ACAGAGATGTTATCTGATGACCAACACCCCAAAATCCATACATATCCCTTTTGGACAA 1692
Db 1144 ACAGAGATGTTATCTGATGACCAACACCCCAAAATCCATACATATCCCTTTTGGACAA 1203
Qy 1693 GACTCGTTCAATGAGCCTTCAGGGAACCAAAATGTGCTCGGCTGACAGTATACGTGGC 1752
Db 1204 GACTCGTTCAATGAGCCTTCAGGGAACCAAAATGTGCTCGGCTGACAGTATACGTGGC 1263
Qy 1753 TTCTTGACAGCGCCACTCGAACCGTGCTACTACTGAGAGACAAATTTGATGACTCTTC 1812
Db 1264 TTCTTGACAGCGCCACTCGAACCGTGCTACTACTGAGAGACAAATTTGATGACTCTTC 1323
Qy 1813 ATCGACCGCTCTTTGAGGTGCTGCTTTGTACCCCTTTGTCAGGTTCTCCAACTGAG 1872
Db 1324 ATCGACCGCTCTTTGAGGTGCTGCTTTGTACCCCTTTGTCAGGTTCTCCAACTGAG 1383
Qy 1873 AGAAACCTCCTGATCTTAGTAAGGCT 1899
Db 1384 AGAAACCTCCTGATCTTAGTAAGGCT 1410

RESULT 11

ADN11987
ID ADN11987 standard; DNA; 1362 BP.

AC ADN11987;

DT 17-JUN-2004 (first entry)

DE AtNHX1 mutant encoding sequence #4.

XX salt tolerance; Na⁺/H⁺ transporter polypeptide; AtNHX1; ds.

XX Synthetic.

XX WO2004007668-A2.

XX 22-JAN-2004.

XX 09-JUL-2003; 2003WO-US021549.

XX 12-JUL-2002; 2002US-0395662P.

XX (REGC) UNIV CALIFORNIA.

XX Shi H, Blumwald E;

XX WPI; 2004-122911/12.

XX P-PSDB; ADN11988.

XX Enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na⁺/H⁺ transporter polypeptide.

XX Claim 7; SEQ ID NO 9; 38pp; English.

XX The present invention relates to enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na⁺/H⁺ transporter polypeptide. The AtNHX1 gene confers salt tolerance. The composition and methods are useful in conferring salt tolerance on plants and other organisms. The present sequence represents a mutant AtNHX1 encoding sequence.

XX Sequence 1362 BP; 329 A; 274 C; 305 G; 454 T; 0 U; 0 Other;

Query Match 62.5%; Score 1362; DB 12; Length 1362;
Best Local Similarity 100.0%; Pred. No. 9.9e-298;
Matches 1362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 286 ATGTTGGATTTCTAGTGTGAACTGCTTCTGTTATCGACATCTGATCAGCTTCTGTG 345
Db 1 ATGTTGGATTTCTAGTGTGAACTGCTTCTGTTATCGACATCTGATCAGCTTCTGTG 60
Qy 346 GTTGCCTTGAATCTCTTTGTGTCATTTCTTTGTGCTTGTATTTCTTTGTGCTATCTTTG 405
Db 61 GTTGCCTTGAATCTCTTTGTGTCATTTCTTTGTGCTTGTATTTCTTTGTGCTATCTTTG 120
Qy 406 GAAGAGATAGATGATGAAACGAATCCATCACCCTTGTGTTGATTTGGGCTAGGCACTGGT 465
Db 121 GAAGAGATAGATGATGAAACGAATCCATCACCCTTGTGTTGATTTGGGCTAGGCACTGGT 180
Qy 466 GTTACCATTTTGTGTTAGTAAAGGAAAGAGCTCGCATCTTCTGCTTTTAGTGAAGAT 525
Db 181 GTTACCATTTTGTGTTAGTAAAGGAAAGAGCTCGCATCTTCTGCTTTTAGTGAAGAT 240
Qy 526 CTTTCTTTCATATATCTTTTGCACCCATTTATATCAATGCAGGCTTCAAGTAAAAAAG 585
Db 241 CTTTCTTTCATATATCTTTTGCACCCATTTATATCAATGCAGGCTTCAAGTAAAAAAG 300
Qy 586 AAGCAGTTTTCGCAATTTCTGTAATTTATGCTTTTGGTCTGTTGGGACTATTTATT 645
Db 301 AAGCAGTTTTCGCAATTTCTGTAATTTATGCTTTTGGTCTGTTGGGACTATTTATT 360
Qy 646 TCTTGCAATCATATCTCTAGTGTAACACAGTTCTTTAAGAGTTGGACATTTGGAACC 705
Db 361 TCTTGCAATCATATCTCTAGTGTAACACAGTTCTTTAAGAGTTGGACATTTGGAACC 420
Qy 706 TTTGACTTGGGTGATTATCTTGCTATTGGTGCCATATTTGCTGCAACAGATTCAGTATGT 765
Db 421 TTTGACTTGGGTGATTATCTTGCTATTGGTGCCATATTTGCTGCAACAGATTCAGTATGT 480
Qy 766 ACATCGAGTTTCTGAAATCAAGACGAGACACCTTTCTTTACAGTCTTTGTTATTCGAGAG 825
Db 481 ACATCGAGTTTCTGAAATCAAGACGAGACACCTTTCTTTACAGTCTTTGTTATTCGAGAG 540
Qy 826 GGTGTTGTGAATGATGCAACGTCAGTTGTGCTTCAACCGGATTCAGAGCTTTGATCTC 885
Db 541 GGTGTTGTGAATGATGCAACGTCAGTTGTGCTTCAACCGGATTCAGAGCTTTGATCTC 600
Qy 886 ACTCAGCTAAACCAACGAGCTGCTTTTCTATCTTTGGAACTTCTTGTAATTTGTTCTC 945
Db 601 ACTCAGCTAAACCAACGAGCTGCTTTTCTATCTTTGGAACTTCTTGTAATTTGTTCTC 660
Qy 946 CTAAGTACCTTGTGTTGCTGCAACCGGCTGATAAGTCCGCTATGTTATCAAGAAAGCTA 1005
Db 661 CTAAGTACCTTGTGTTGCTGCAACCGGCTGATAAGTCCGCTATGTTATCAAGAAAGCTA 720
Qy 1006 TACTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTATGGCGTATCTT 1065
Db 721 TACTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTATGGCGTATCTT 780
Qy 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTCACTGTGTTTTTCTGTGGT 1125
Db 781 TCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTCACTGTGTTTTTCTGTGGT 840
Qy 1126 ATTGTGATGTCCTATTCACATGGCAAAATGAAACGAGAGCTTCAAGAAATAACAACAAG 1185
Db 841 ATTGTGATGTCCTATTCACATGGCAAAATGAAACGAGAGCTTCAAGAAATAACAACAAG 900
Qy 1186 CATACCTTTGCAACTTTGTGCTTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 1245
Db 901 CATACCTTTGCAACTTTGTGCTTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 960
Qy 1246 GATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305
Db 961 GATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020

QY 1306 GTGAGCTCAATCTTAATGGGCTCGTTCATGTTGGAGAGCAGCGTTTCGTTCCGTTA 1365
DB 1021 GTGAGCTCAATCTTAATGGGCTCGTTCATGTTGGAGAGCAGCGTTTCGTTCCGTTA 1080
QY 1366 TCGTTTCTAATCTTAATGGGCTCGTTCATGTTGGAGAGCAGCGTTTCGTTCCGTTA 1425
DB 1081 TCGTTTCTAATCTTAATGGGCTCGTTCATGTTGGAGAGCAGCGTTTCGTTCCGTTA 1140
QY 1426 GTTGTGATTTGGTGGTCTGTTCTCATGAGAGGTCGTATCTATGCTCTTTCGATACAAC 1485
DB 1141 GTTGTGATTTGGTGGTCTGTTCTCATGAGAGGTCGTATCTATGCTCTTTCGATACAAC 1200
QY 1486 AAGTTTCAAGGGCCGGGCAACAGATGTACGGGGGAATGCAATCATGATCAGAGTAAG 1545
DB 1201 AAGTTTCAAGGGCCGGGCAACAGATGTACGGGGGAATGCAATCATGATCAGAGTAAG 1260
QY 1546 ATAACTCTCTGCTCTTTTATGACAGAGTGGTGTGGTATGCTGACCAACCACTCATAAGC 1605
DB 1261 ATAACTCTCTGCTCTTTTATGACAGAGTGGTGTGGTATGCTGACCAACCACTCATAAGC 1320
QY 1606 TACCTATTACCGCACAGAACGCCACCAAGAGCATGTTATCT 1647
DB 1321 TACCTATTACCGCACAGAACGCCACCAAGAGCATGTTATCT 1362

RESULT 12

ADN11993
ID ADN11993 standard; cDNA; 1323 BP.

AC ADN11993;

DT 17-JUN-2004 (first entry)

NDL-3 encoding sequence.

salt tolerance; Na⁺/H⁺ transporter polypeptide; AtNHX1; ss.

Saccharomyces sp.

WO2004007668-A2.

22-JAN-2004.

09-JUL-2003; 2003WO-US021549.

12-JUL-2002; 2002US-0395662P.

(REGC) UNIV CALIFORNIA.

Shi H, Blumwald E;

WPI; 2004-122911/12.

P-PSDB; ADN11994.

Enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na⁺/H⁺ transporter polypeptide.

Claim 7; SEQ ID NO 15; 38pp; English.

The present invention relates to enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na⁺/H⁺ transporter polypeptide. The AtNHX1 gene confers salt tolerance. The composition and methods are useful in conferring salt tolerance on plants and other organisms. The present sequence represents NDL-3 encoding sequence.

Sequence 1323 BP; 326 A; 290 C; 297 G; 410 T; 0 U; 0 Other;

Query Match

Best Local Similarity 99.9%; Score 1320.4; DB 12; Length 1323;

Matches 1321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 578 TAAAGAGAGCAGTTTTCGCAATTCGTGACTATTATGCTTTTGGTCTGTGGGA 637

DB 2 TGAAGAGAGCAGTTTTCGCAATTCGTGACTATTATGCTTTTGGTCTGTGGGA 61
QY 638 CTATTTATTTCTGACAAATCATATCTCTAGGTGTAAACAGTTCCTTTAAGAGTTGACAA 697
DB 62 CTATTTATTTCTGACAAATCATATCTCTAGGTGTAAACAGTTCCTTTAAGAGTTGACAA 121
QY 698 TTGGAACCTTTGACCTTTGGGTGATTAATCTTGTCTATTTGGTGCCATATTTGCTGCAACAGATT 757
DB 122 TTGGAACCTTTGACCTTTGGGTGATTAATCTTGTCTATTTGGTGCCATATTTGCTGCAACAGATT 181
QY 758 CAGTATGTACACTGACAGTTTCTGAATCAAGACGAGACACCTTTTGTCTTTACAGTCTTTGTAT 817
DB 182 CAGTATGTACACTGACAGTTTCTGAATCAAGACGAGACACCTTTTGTCTTTACAGTCTTTGTAT 241
QY 818 TCGGAGAGGTTGTGTAATGATGCAACGTCTAGTGTGTCTTCAACGGGATTCAGAGCT 877
DB 242 TCGGAGAGGTTGTGTAATGATGCAACGTCTAGTGTGTCTTCAACGGGATTCAGAGCT 301
QY 878 TTGATCTCACTCACTTAAACCAAGAGTGTCTTTTTCATCTTCTTGGAAACTTCTTCTATT 937
DB 302 TTGATCTCACTCACTTAAACCAAGAGTGTCTTTTTCATCTTCTTGGAAACTTCTTCTATT 361
QY 938 TGTTCCTCCTAAGTACCTTTGCTGTGCTGCAACCGGTCTGATAAGTGCCTATGTTATCA 997
DB 362 TGTTCCTCCTAAGTACCTTTGCTGTGCTGCAACCGGTCTGATAAGTGCCTATGTTATCA 421
QY 998 AGAAGCTATCTTTGGAGGCACTCAACTGACGGAGAGGTTGCCCTTATGATGCTTATGG 1057
DB 422 AGAAGCTATCTTTGGAGGCACTCAACTGACGGAGAGGTTGCCCTTATGATGCTTATGG 481
QY 1058 CGTATCTTTCTTATATGCTTGTGAGCTTTTCGACTTTGACGGGTATTCCTCACTGTGTTTT 1117
DB 482 CGTATCTTTCTTATATGCTTGTGAGCTTTTCGACTTTGACGGGTATTCCTCACTGTGTTTT 541
QY 1118 TCTGTGTTATGTTGATGCTCCATTAACATGCACAATGTAAACGGAGAGCTCAAGAATAA 1177
DB 542 TCTGTGTTATGTTGATGCTCCATTAACATGCACAATGTAAACGGAGAGCTCAAGAATAA 601
QY 1178 CAACAAAGCATACCTTTGCAACTTTGTCAATTTCTTGGGAGACATTTATTTCTTGTATG 1237
DB 602 CAACAAAGCATACCTTTGCAACTTTGTCAATTTCTTGGGAGACATTTATTTCTTGTATG 661
QY 1238 TTGGAATGGATGCTTGGACATTTGAACAGTGGAGATCCGTGAGTGACACACCGGGAACAT 1297
DB 662 TTGGAATGGATGCTTGGACATTTGAACAGTGGAGATCCGTGAGTGACACACCGGGAACAT 721
QY 1298 CGATCGCAGTGAGCTCAATCTTAATGGGTCTGGTCAATGGTTGGAAAGAGCAGGTTCTGCT 1357
DB 722 CGATCGCAGTGAGCTCAATCTTAATGGGTCTGGTCAATGGTTGGAAAGAGCAGGTTCTGCT 781
QY 1358 TTCCGTTATCGTTTCTATCTTAACCTTTAGCAAGAAATCAAGCGGAGAAATCAACTTTA 1417
DB 782 TTCCGTTATCGTTTCTATCTTAACCTTTAGCAAGAAATCAAGCGGAGAAATCAACTTTA 841
QY 1418 ACATCAGGTTGTGATTTGGTGGTCTGGTCTCATGAGAGGTCGTCTATCTATGGCTCTTG 1477
DB 842 ACATCAGGTTGTGATTTGGTGGTCTGGTCTCATGAGAGGTCGTCTATCTATGGCTCTTG 901
QY 1478 CATACAACAGTTTCAAGGGCCGGGCAACAGATGTAGCGGGGAATGCAATCATGATCA 1537
DB 902 CATACAACAGTTTCAAGGGCCGGGCAACAGATGTAGCGGGGAATGCAATCATGATCA 961
QY 1538 CGAGTACCATTAATCTCTCTCTTTTACACAGTGGTGTGGTGTGCTGACCAACCAAC 1597
DB 962 CGAGTACCATTAATCTCTCTCTTTTACACAGTGGTGTGGTGTGCTGACCAACCAAC 1021
QY 1598 TCATAAGTACTCTATTAACCGCACCAAGAACCGCACACAGAGCATGTTATCTGATGACAA 1657
DB 1022 TCATAAGTACTCTATTAACCGCACCAAGAACCGCACACAGAGCATGTTATCTGATGACAA 1081
QY 1658 CCCCAAAATCATATATCTTTTGGTGGAGAGAGTCTGTTCTATGAGCTTTCAGGCTTCAGGA 1717


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Db 1490 TAGTTGACCTAGTAGCTCCGATGCTTCTAAATGCACTACTCACACCGTCCATCACT 1549
Qy 1787 ACTGGAGACAATTTGATGACTCTCTTCATGCGACCCGCTTTTGGAGGTCGTGGCTTTGTAC 1846
Db 1550 ATTGGCGCAATTCGATGACTCTCTTCATGCGCCGCTTTTGGTGGCGGGTTTGTAC 1609
Qy 1847 CTTTGTTCAGGTTCTCCAACTGAGAGAAACC 1880
Db 1610 CTTTGTCCGGGTTACCTACTGAACAAGCAC 1643

RESULT 15
AAF75765
ID AAF75765 standard; DNA; 2553 BP.
XX
AC AAF75765;
XX
DT 14-MAY-2001 (first entry)
XX
DE Gene regulating the pH of vacuoles.
XX
KW Vacuole pH regulation; flower colour; da.
XX
OS Nierembergia hybrida.
XX
PN WO200114560-A1.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-JP005722.
XX
PR 24-AUG-1999; 99JP-00236800.
XX
PA (SUNR ) SUNTORY LTD.
XX
PI Iida S, Tanaka S, Inagaki Y;
XX
DR WPI; 2001-191648/19.
DR P-PSDB; AAB73253.
XX
PT Morning glory-originated gene encoding a protein with pH regulation
PT activity in vacuoles, useful in controlling flower color to give new
PT breeds of colorful plants for cut flowers, particularly applicable in
PT horticulture.
XX
PS Example 7; Page 45-49; 68pp; Japanese.
XX
CC The present sequence is a gene, which encodes a protein with vacuolar pH
CC regulatory activities. The gene enables flower colour to be controlled
CC via regulation of the vacuolar pH, colours can range from blue to red in
CC colour spectrum. The gene is useful in controlling flower colour to give
CC new breeds of colourful plants for cut flowers, particularly applicable
CC in horticulture
XX
SQ Sequence 2553 BP; 666 A; 487 C; 535 G; 865 T; 0 U; 0 Other;

Query Match 37.7%; Score 821.2; DB 4; Length 2553;
Best Local Similarity 70.3%; Pred. No. 2.1e-175;
Matches 1115; Conservative 0; Mismatches 468; Indels 3; Gaps 1;

Qy 289 TTGGATTCTAGTGTGCAAACTCCCTTCGTTATCGACATCTGATCACGCTTCTGTGGTT 348
Db 543 TTTGGGACTCTGCTGGGAAGATGAACTTAACTTCTGATCATCAATCAGTGGTG 602
Qy 349 GCCTTGAATCTTTGTGCACTTCTTTGTGCTGATGTTCTTGTGCTATCTTTGGAA 408
Db 603 TCGGTAACTTTTGTGCACTTATTTGGCGGTATTTGATCGGTCACTTTATTTGGAG 662
Qy 409 GAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 468
Db 663 GAAAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 722

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Qy 469 ACCATTTTGTGATTAGTAAAGGAAAAAGCTCCGATCTTCTCGTCTTTAGTGAAGATCTT 528
Db 723 ATCAATTTCTAATAAATGAGGAGAAAGAACTCAATATTTTAGTGTTCAGCGAAGATCTT 782
Qy 529 TTCTTCATATATCTTTTGGCCACCATTATATCAATGCAAGGCTTTCAAGTAAAGAAAGAA 588
Db 783 TTCTTCATTTACCTTCTTCCACCGATCAATTTTAAATGCTGGGTTCCAGGTGAAAGAA 842
Qy 589 CAGTTTTCGCAATTTCCGCACTATATATGCTTTTGGTGTCTGTGGGATATATTTCT 648
Db 843 TCATTTCTCCGCAATTTTCACTATCATGCTCTTTGGGCGAGTTGGCACCTTGATATCG 902
Qy 649 TGCACAAATCATATCTCTAGGTGTAAACACAGTTCTTTAAGAGTTGGACATTTGACCTTT 708
Db 903 TTCAATTTATATATCAGCGGTGCTATTTGGCAATTTCAAGAAATGGAATATTTGACACCTT 962
Qy 709 GACTTGGGTGATTATCTTGTCTATTGGTGCCATATTTGCTGCAACAGATTCAGTATGTACA 768
Db 963 GAAATTTGGAGATTACCTTGCATTTGGAGCAATCTTTGCTGCAACAGATTTCTGTATGCACC 1022
Qy 769 CTGAGGTTTCTGAATCAAGACGAGACACCTTTTACAGTCTTGTATTCGGAGAGGTT 828
Db 1023 TTACAAAGTCTTAATCAGGAAGAAACACCGTTATTGTACAGTCTAGTGTTTGGAGAAGT 1082
Qy 829 GTTGTGAATGATGCAACAGTGTGCTTTCACGCGGATTCAGAGCTTTGTATCTCACT 888
Db 1083 GTTGTGAATGATGCCACATCTGTAGTGTCTTCAATGCTGTCCAGAACTTTGACTTATCT 1142
Qy 889 CACCTAAACCAAGAGCTGCTTTTCATCTCTTGGAACTTCTTGTATTTGTTCTCCTA 948
Db 1143 CATATCAGCACAGGCAAGCTCTGCAATTAATTTGGAACCTTTCTATACCTTTTGGCTCG 1202
Qy 949 AGTACCTTGTGCTGCTGCAACCGGTCTGATAAGTCCGTATGTTATCAAGAAAGCTATAC 1008
Db 1203 AGCACCTTCTAGGGGTGCTGTGGCTACTAAGTGCTTTTATAATTAAGAAACTCTAC 1262
Qy 1009 TTTGGAAGGCACTCAACGACGAGAGGTTGCCCTTATGATGCTTATGGGCTATCTTCT 1068
Db 1263 TTTGGAAGGCACTCGATCGTGGGTTGCTATTAATGATCTATGCGGCTACCTATCA 1322
Qy 1069 TATATCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTCACTGCTGTTTTTCTGTGGTATT 1128
Db 1323 TACATCTTGTGCAATTTATTTCTATTTAAGTGGAACTCTCACTGTGTTTTTCTGTGGGATC 1382
Qy 1129 GTGATGTCCCAATTACACATGCGCAATGTAAACGAGAGCTCAAGAAATFAACAAAGCAT 1188
Db 1383 GTGATGTCTCACTATACCTGGCATAATGTCACTGAGAGCTCAAGAGTCACTACCAAGCAC 1442
Qy 1189 ACCTTTGCAACTTTTGTCTTTCTTGGGAGACATTTATTTTCTTGTATGTTGGAATGGAT 1248
Db 1443 ACGTTTGTCTACATTTATTTATTTGCTGAAATATTCATATTTCTTATGTTGGTATGGAT 1502
Qy 1249 GCCTTGGACATTTGACAAAGTGGAGATCCGTCAGTGACACACCGGGAACATCGATCGCAGTG 1308
Db 1503 GCTTTGGACATTTGAGAAAGTGGAAAGTTTGAAGGACAGCCCCGGAACATCANTTAAGGTC 1562
Qy 1309 AGCTCAATCTTAATGGGTCTGGTCTAGTGTGGAAGAGACGCTTCGTTCTTTCGCTTATCG 1368
Db 1563 AGCTCAATCTCTAGTCTGTGTTTGGTGGAGGGGAGCCCTTTGTTTCCCTTGTCA 1622
Qy 1369 TTTCTATCTTAACCTTAGCCAAAGAAATCAAGCGGAGAAATCACTTTTAAATGATGAGGTT 1428
Db 1623 TTCTTGTCAACTTTGACCAAGAAATCTCTGAGGACAGATTAAGCTTTTAAACGAGGTT 1682
Qy 1429 GTGATTTGGTGTCTGGTCTCATGAGAGGTCGTATCTATGCTCTTGCATACACAAG 1488
Db 1683 ACAATATGTTGGGCTGGGCTTATGCGAGGTGCTTTCTATGGCCCTTGTCTTAAATCAG 1742
Qy 1489 TTTTAAAGGCGCGGGCACACAGATGTACCGGGAATGCAATCATGATCAGAGTACGATA 1548
Db 1743 TTTTACAGGGGAGGTCATCTACTAGTTACGTGCCAATGCAATATGATCAGAGTACTATC 1802
Qy 1549 ACTGTCTGCTTTTATAGCACAGTGGTGTGTTGGTATGCTGACCAAAACC---ACTCATAGC 1605

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[illegible]

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-617-623-1
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
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4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 2 | 630.6 | 29.0 | 3272 | 3 | AY109416 | AY109416 Zea mays |
| 3 | 595.6 | 27.3 | 651 | 6 | C99909 | C99909 C99909 Arab |
| 4 | 487.2 | 22.4 | 834 | 6 | CA767092 | CA767092 AF53-Rpf |
| 5 | 478.8 | 22.0 | 1449 | 9 | CL973674 | CL973674 OSIFCC024 |
| 6 | 435.8 | 20.0 | 483 | 5 | BP570332 | BP570332 BP570332 |
| 7 | 432.8 | 19.9 | 966 | 7 | CK260919 | CK260919 EST706997 |
| 8 | 432 | 19.8 | 433 | 1 | AV792419 | AV792419 AV792419 |
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| 21 | 401.4 | 18.4 | 804 | 7 | CO100982 | CO100982 GR_Eb002 |
| 22 | 400.8 | 18.4 | 615 | 5 | BQ589958 | BQ589958 S01538-0 |
| 23 | 397.8 | 18.3 | 404 | 5 | BP609318 | BP609318 BP609318 |
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Query Match

30.8%; Score 671.6; DB 3; Length 2080;

ALIGNMENTS

RESULT 1
LOCUS AY105332 2080 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PC0131050 mRNA sequence.
ACCESSION AY105332
VERSION AY105332.1 GI:21208410
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 2080)
AUTHORS Hayney, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whittitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 2080)
AUTHORS Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

source

Location/Qualifiers
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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont accessions; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

30.8%; Score 671.6; DB 3; Length 2080;

| | | | | | | | | | |
|---|--|--|------|--|--|--|--|--|--|
| Best Local Similarity 65.5%; Pred. No. 7.4e-149; Matches 1029; Conservative 0; Mismatches 534; Indels 7; Gaps 3; | | | | | | | | | |
| QY | 318 | GTATTCGACATCTCATCAGCGTCTCTGTGGTTCGAATCTCTTCTGTCACATCTCTTTG | 377 | | | | | | |
| Db | 225 | GCTCTCGGTCTCGATCAGACGCCATCTGCTCAATTAACATCTTCACTCGCGTCTGCTG | 284 | | | | | | |
| QY | 378 | TGCTGTATTGTTCTTGGTCATCTTTTGAAGAGATAGATGGAACGAATCCATCAC | 437 | | | | | | |
| Db | 285 | CAGTCGATTGTATCGGCCACTTGTCTGAAGGAAACCGATGGTGAACGAGTCCATCAC | 344 | | | | | | |
| QY | 438 | CGCCTTGTATGGGCTAGGCACTGTGTATCAATTTTGTGTATAGTAAAGAAAG | 497 | | | | | | |
| Db | 345 | CGCGCTTGTATGGGCTCATCACCGGAGGCGTCACTCTGCTGTTACTAATGGGACAA | 404 | | | | | | |
| QY | 498 | CTCGCATCTCTCTGCTTTAGTGAAGATCTTTTCTTCATATATCTTTTGCACCCATAT | 557 | | | | | | |
| Db | 405 | CTCAGGATCTTGTGTTAGCGAGGACCTGTTTTTTCATATATTTACTTCCGCGATAAT | 464 | | | | | | |
| QY | 558 | ATTCAATGCAAGGTTTCAAGTAAAGAAAGACGAGTTTTCGCAATTTTCGTGACTATTAT | 617 | | | | | | |
| Db | 465 | CTTCAATGCCGGTTTCAAGTAAAGAAAGCAATTTCTTCGCAACTTTTATAAGGATTAT | 524 | | | | | | |
| QY | 618 | GCCTTTTGGTCTGTTGGGACTATATTTCTTGGCAATCATATCTCTAGGTGTAAACA | 677 | | | | | | |
| Db | 525 | TTTGTGTTGGTCTATTGGGACTCTGATTCTCTTTGTAATAATCTCTCTTGGTCTATGGG | 584 | | | | | | |
| QY | 678 | GTTCTTTAAGAAGTTGACATCTGCACTTTGACTTGGGTGATTACTTCTGCTATTCGTGC | 737 | | | | | | |
| Db | 585 | GTTGTTCAAGAACTTGATGTTGGTCCACTGAGACTTGGGACTATCTTGGCAATTTGGTGC | 644 | | | | | | |
| QY | 738 | CATATTTGTCGCAACGATTTCAGTATGTATACCTGCAAGTTCTGAAATCAAGACGACACC | 797 | | | | | | |
| Db | 645 | TATTTTCTCGGCAACAGATTCTGTTGACCTTTACAGGTGCTTAAACGAGATGAACACC | 704 | | | | | | |
| QY | 798 | TTTGTCTTACAGCTTGTATTTCGAGAGGGTGTGTAATGATGCAAGCTCAGTTGTGGT | 857 | | | | | | |
| Db | 705 | CCTACTCTATAGTCTAGTTTGGTGAAGGTGTTGTAATGATGCCACATCTCTTGTGCT | 764 | | | | | | |
| QY | 858 | CTTCAAGCGCATTCAGAGCTTTCATCTCACTCACTTAAACCAAGAGCTGCTTTTCATCT | 917 | | | | | | |
| Db | 765 | CTTCAATGCAATTTGAACCTTGATATGTAATATTTTGTATGCTATTGTTCTGTGAAATTT | 824 | | | | | | |
| QY | 918 | TCTTGAAACTCTTGTATTGTTTCTCTCAAGTACCTTCTGTTGGTCTGCAACCGGTCT | 977 | | | | | | |
| Db | 825 | CGTCCGAAATTTCTCTACTTGTCTTCAACGACCATACTTTGGAGTAGCTACCGGGTT | 884 | | | | | | |
| QY | 978 | GATAAGTGCCTATGTTATCAAGAGCTATATCTTTGAAGGCACTCAACTGACCGAGGTT | 1037 | | | | | | |
| Db | 885 | GCTTAGTGCATACATTATCAAGAGCTCTGTTTGGCAGACATTCAACTGATAGAGAAT | 944 | | | | | | |
| QY | 1038 | TGCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTGTGAGCTTTTCGACTTGAG | 1097 | | | | | | |
| Db | 945 | TTCTATCATGATACTCATGSCATACCTTTCAATCATGATATCATGCTGTGTGACCTGAG | 1004 | | | | | | |
| QY | 1098 | CGGTATCTCTCACTGTGTTTCTCTGTTGTAATGATGTCCTTCAATGATGCAACAATGT | 1157 | | | | | | |
| Db | 1005 | TGGAATTTCTTACTGCTTCTCTCTGGAATAGTAAATGTCAATTCACATTTGCAATAATGT | 1064 | | | | | | |
| QY | 1158 | AACGGAGAGCTCAAGATTAACAACAAGCATCTTTTGGCACTTTGCTCATTTCTTTCGGA | 1217 | | | | | | |
| Db | 1065 | GACAGAAAGTTCTAGGGTTACCAACCAAGCATCTTTTGAACCTTTATCATTCATTGSCAG | 1124 | | | | | | |
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| Db | 1185 | TAGTAGCAGTCTTAAGAAACCAATTCGGTTTAAAGTCAATTTATTTTGGGCTTGGTTATGG | 1244 | | | | | | |
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| | | | | | | | | | |
| Db | 1245 | TTGGAAGAGCGGCAATTTGTTATTTCCCTTTTGTGCTTCTTATCCAACTAAGCAAAAGGAGG | 1304 | | | | | | |
| QY | 1397 | AAAGCGAGAAATCAACTTTTAAATGTCAGAGTTGATTTGGTCTGCTCATCAGAG | 1456 | | | | | | |
| Db | 1305 | CCGCTCCAAGATCTCTTCAAGCAAAAGTAATCATATGTTGGTGGTCTCATGAGAG | 1364 | | | | | | |
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| Db | 1365 | GAGCAGTGTCAATTTGGCTTGGCTATATAAAGTTTACAGCATCTGCTCACACTGAAGTGC | 1424 | | | | | | |
| QY | 1517 | GCGGGAATGCAATCATGATCAGAGTACAGTAACTGTCTGCTTTTATAGACAGTGGTGT | 1576 | | | | | | |
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| QY | 1577 | TTGGTATGCTGACCAACCACTCATAAAGCTACTATTACCGCACCAAGACGCCACCA | 1636 | | | | | | |
| Db | 1485 | TGGGCTGCTGAGAGCGGCTGCTCAGTCTCTCATCCAC-CAAGGACTGGACTGAAC | 1543 | | | | | | |
| QY | 1637 | GCATGTTATCTGATGACACACCCCAAAATCCATACATATCCCTTTGTTGGACCAAGACT | 1696 | | | | | | |
| Db | 1544 | ACGTGCTCTCTCTCTCAAGCCAGTCTATGCTGGACCCCACTCTTACTAGCATGA----- | 1598 | | | | | | |
| QY | 1697 | CGTTCATTGAGCCTTCAGGGAACCAATGTGCTCGGCTGACAGTATACGTGGCTTCT | 1756 | | | | | | |
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| QY | 1757 | TCACACGGCCCACTCGAACCGTGCAATTAATCTACTGAGAGCAATTTGATGACTCTTCATGC | 1816 | | | | | | |
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| QY | 1817 | GACCGCTCTTTTGGAGGTGCTGCTTTTGTACCTTTTGTCCAGGTTCTCCAACTGAGAGAA | 1876 | | | | | | |
| Db | 1719 | GCCCGGTGTTGGGGGCGAGGTTTCGTCCTTTTGTGCTGTTCCGCGTGGAGAGA | 1778 | | | | | | |
| QY | 1877 | ACCCTCCTGA | 1886 | | | | | | |
| Db | 1779 | GTGTCCTCTGA | 1788 | | | | | | |
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| RESULT 2 | | | | | | | | | |
| AY109416 | | | | | | | | | |
| LOCUS | AY109416 | | | | | | | | |
| DEFINITION | Zea mays CL694_1 mRNA sequence. | | | | | | | | |
| ACCESSION | AY109416 | | | | | | | | |
| VERSION | AY109416.1 | GI:21213132 | | | | | | | |
| KEYWORDS | HTC | | | | | | | | |
| SOURCE | Zea mays | | | | | | | | |
| ORGANISM | Zea mays | | | | | | | | |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. | | | | | | | | |
| REFERENCE | 1 (bases 1 to 3272) | | | | | | | | |
| AUTHORS | Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. | | | | | | | | |
| TITLE | Maize Mapping Project/buPont Consensus Sequences for Design of Overgo Probes | | | | | | | | |
| JOURNAL | Unpublished (2002) | | | | | | | | |
| REFERENCE | 2 (bases 1 to 3272) | | | | | | | | |
| AUTHORS | Coe, E.H. | | | | | | | | |
| TITLE | Direct Submission | | | | | | | | |
| JOURNAL | Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA | | | | | | | | |
| COMMENT | If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu. | | | | | | | | |
| FEATURES | Location/Qualifiers | | | | | | | | |
| source | 1..3272 | | | | | | | | |
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| | /mol_type="mRNA" | | | | | | | | |

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| DEFINITION | C99909 Arabidopsis thaliana library (Motohashi R) Arabidopsis thaliana cDNA clone 65, mRNA sequence. | | | | |
| ACCESSION | C99909 | | | | |
| VERSION | C99909.1 | GI:4714029 | | | |
| KEYWORDS | EST. | | | | |
| SOURCE | Arabidopsis thaliana (thale cress) | | | | |

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ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 651)
Motohashi, R., Shinozaki, K. and Yamaguchi-Shinozaki, K.
Arabidopsis thaliana YAC C1C3B1 region specific cDNA, clone 2
Unpublished (1999)
Contact: Motohashi R
Laboratory of Plant Molecular Biology
Institute of Physical and Chemical Research (RIKEN)
3-1-1, Koyadai, Tsukuba 305-0074, Japan
Tel: +81-298-36-4359
Email: motohashi@rtc.riken.go.jp.
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DB 61 ACACCGGGAACATCGATCGCAGTGAGCTCAATCTAATGGTCTGGTCTGATGGTGAAGA 120
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DB 121 GCAGCGTTCGTTTCGGTTATCGTTTCTAATCTAATCCCAAGAAAGATCAAAACGAG 180
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DB 181 AAATCAACTTAAACATGACGAGTTGATTTGGTGGTCTGATGAGAGGTGCTGTA 240
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DB 241 TCTATGGCTCTTGATACAAAGTTTACAAAGGCGCGGCACACAGATGTACCGGGAAT 300
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DB 361 CTGACCAAAACCACTCAATGCTACCTATTACCGCACAGAACGCCACACGAGCATGTTA 420
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DB 421 TCTGATGACAAACCCCAAAATCCATACATATCCCTTTGTTGGAACAAGAC-CGTTCAAT 479
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DB 480 GAGCCTTCAGGGAACCAACATGTCGCTCGCCTGACAGTATACGTGGCTTCTTGACACGG 539
QY 1765 CCCATCGAACCGTGCAATTAAGTCTGAGACAAATTTGATGACTCCCTCATGCGACCCGT 1823
DB 540 SCCCTCSAACCGTGCAATTAAGTCTGAGACAAATTTGATGACTCCCTCATGCGACCCGT 599
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DB 600 CTTTGGGAGGTCGTGGCTTTGACCTTTGTTTCCARGGTTCTCCAACTGAR 651

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CA767092 834 bp mRNA linear EST 08-JAN-2003
AF53-Rpf 13 P08 T7 032.ab1 IRRI Drought Stress Panicle Library
Oryza sativa (indica cultivar-group) cDNA clone C0004976 5'. Similar
to Sodium/hydrogen exchanger 6 (Na(+)/H(+) exchanger 6) (NHE-6),
mRNA sequence.
CA767092
CA767092.2 GI:27549114
EST.
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 834)
Bennett, J., Arumugam, K., Lafitte, R., Wen, J., Rudd, S. and
Bruskiewich, R.W.
IRRI Drought Stress Panicle cDNA Library
Unpublished (2002)
On Dec 2, 2002 this sequence version replaced gi:25996347.
Contact: Richard Bruskiewich
Bionetrics and Bioinformatics Unit
International Rice Research Institute
DAPO 7777, Metro Manila, Philippines
Tel: +63-2-845-0563
Fax: +63-2-845-0606
Email: r.bruskiewich@cgiar.org
International Rice Information System (IRIS);
http://www.iris.irri.org/; D0204975
Assignment of putative function to the sequence by S. Rudd of the
Munich Information Center for Protein Sequences
(http://mips.gsf.de)
Plate: 13 row: P column: 08.
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ORIGIN
    Query Match      22.4%; Score 487.2; DB 6; Length 834;
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QY 760 GPATGTACATCGAGGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGATTC 819
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QY 940 TTTCTCTTAAGTACTTCTGCTGGTCTGCAACCGGTCTGATAAGTGCCTATGTTATCAAG 999
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DB 242 AAGCTATATCTTTGAAGGCACTTACTGACCGTGGTTCCTTATGATGCTATGCT 301

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Db 849 -----ACCTGCAAAATCAATGGGATAAGCTCAATTTTGTAGATTGGT 893
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RESULT 6
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LOCUS BP570332 483 bp mRNA linear EST 20-JUN-2004
DEFINITION BP570332 RAFL14 Arabidopsis thaliana cDNA clone RAFL14-72-D17 3',
mRNA sequence.
ACCESSION BP570332
VERSION BP570332.1 GI:48986098
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE
AUTHORS Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
TITLE Functional annotation of a full-length Arabidopsis cDNA collection
JOURNAL Science 296 (5565), 141-145 (2002)
MEDLINE 21932900
PUBMED 11910074
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
reversed clone; Please visit our web site

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FEATURES
source
Location/Qualifiers
1..483
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(http://pfweb.gsc.riken.go.jp/) for further details.

ORIGIN
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Best Local Similarity 97.9%; Pred. No. 9.1e-93;
Matches 473; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

QY 1670 TACATATCCCTTTGTTGGACCAAGACTCGTTCAATTGAGCCTTCAGGGAACCAATGTG- 1728
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QY 1908 AGTGAAGAAAGCTTTGATTTTGGTGAAGAAAGGCTGATTCAAATTAATGCTTTTG 1967
Db 243 AGTGAAGAAAGCTTTGATTTTGGTGAAGAAAGGCTGATTCAAATTAATGCTTTTG 184
QY 1968 -TGTAATTTATCATTTGTAATTTGTTGTCGAGACAGAAATCTGCTCAAGTTTGA 2026
Db 183 CTGTAATTTATCATTTGTAATTTGTTGTCGAGACAGAAATCTGCTCAAGTTTGA 124
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QY 2147 TCG 2149
Db 3 TCG 1

RESULT 7
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LOCUS BP5706919 966 bp mRNA linear EST 03-AUG-2004
DEFINITION BP5706919 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone FOAB652 5' end, mRNA sequence.
ACCESSION BP5706919
VERSION BP5706919.1 GI:39817897
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
REFERENCE
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamecheva, S.A. and Baker, B.
TITLE Generation of ESTs from abiotic stressed potato tissue
JOURNAL Unpublished (2003)
COMMENT Other ESTs: BP5706998
Contact: Robin Buell

```

The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potatoc-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GNG ACA CTA TAG.
Location/Qualifiers
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/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
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grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN

Query Match 19.9%; Score 432.8; DB 7; Length 966;
Best Local Similarity 66.8%; Pred. No. 5.3e-92;
Matches 647; Conservative 0; Mismatches 317; Indels 4; Gaps 2;
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DB 1 GGTGTTGTGAATGATGCAAGCTCAGTTGGTCTTCAACCGGATTCAGAGCTTTGATCTC 60
QY 886 ACTCAGCTAAACCAAGGCTGCTTTTCATCTTTGGAACTCTTGTATTTGTTCTC 945
DB 61 TCTCATATCAACCAAGGCTGCTTTTCATCTTTGGAACTCTTGTATTTGTTCTC 120
QY 946 CTAAGTACCTTGGTGTGTCGACCGGCTGATAGTGGTATGTTATCAGAGACTA 1005
DB 121 TCAGAGCACCCTCTAGGGGTTGTACTGGTCTACTGAGCGCTATATAATTAAGAACTC 180
QY 1006 TACTTTGGAGGCACTCAACTGACCGAGGTTGCCCTTATGATGCTTATGGGCTATCTT 1065
DB 181 TACTTTGGAGGCACTCAACTGACCGGTTGCCCTTATGATGCTTATGGGCTATCTT 240
QY 1066 TCTTATATGCTTGTGAGCTTTTCGACTTCGAGCGGTATCTCTACTGTGTTTCTGTGGT 1125
DB 241 TCATACATGCTTGTGATATTTCTATTAAAGTTCAATCTCTACTGTGTTTCTCGGG 300
QY 1126 ATTGTGATGTCCTATACATGCGCAATGTAAACGAGAGCTCAAGAAATACAAAG 1185
DB 301 ATTGTGATGTCCTACTACACCTGGCATAATGTGACTGAGAGCTCAAGAGTCAACCAAG 360
QY 1186 CATACCTTGCACCTTGTCTATCTTCGGGAGACATTTATTTCTGTATGTTGGAATG 1245
DB 361 CATGCTTTTGCTACATTTATTTATGCTGGAATATTTCA--TTCTTTATGTTGGTATG 418

QY 1246 GATGCTTTGGACATTCACAAGTGGAGATCGGTGAGTGACACACCGGGAACATCGATCGCA 1305
DB 419 GATGCTTTGGACATTCACAAGTGGAGATTTGTAAAGCGACCGCCACAATTCAGTTTCAG 478
QY 1306 GTGAGCTCAATCTTAATGCTGCTGATGTTGGAAAGAGCAGCGTTTCGTTCTTCCGTTA 1365
DB 479 GTTAGCTCCATCTCTGTTGGGCTCTGTTTGGTGGAAAGGCGAGCATTTGTTTCCCTG 538
QY 1366 TCGTTTCTATCTAATCTTAGCCAAAGAAATCAAAAGGAGAGAAATCAATTTTAAATGCGAG 1425
DB 539 TCATTTTGTCCAACTTGATGAAGAGTCTCCGAGGAGAGGATTAGCTTTAAACCAAGCA 598
QY 1426 GTTGTGATTTGGTGGTCTGCTCATGAGAGGTGCTGTATCTATGCTCTTGTGATCAAC 1485
DB 599 ATTATAATATGTTGGGCTGGACTTATGCGAGGTGCTGTTTTCAGTGGCTCTTGTCTTAAT 658
QY 1486 AGTTTACAAAGGCGCGGCGACACAGATGTACCGGGAATGCAATCATGATCAGAGTACG 1545
DB 659 CAGTTTACAGGGGAGGCCATCTAGTTAGTGCCAGGCCATATGATCACAAGTACT 718
QY 1546 ATAACCTGCTGCTTTTTTAGCAGAGTGGTGTGTTGGTATGCTGACCAAAACCATCATAAGC 1605
DB 719 ATCAGCTGTTGCTCTTTTCAGCAGCGGGTTTTCGGGTGATGACAAAACCTTTAATTTAGA 778
QY 1606 TACCTATTACCGCACAGAACGCCACACGAGCATGTTATCTGATCA--CAACACCCCA 1663
DB 779 TTATTGCAACCTTCATCTAAACATCTTGAGCAGAAATGATCTCTTCTGAACCGAGACCCCA 838
QY 1664 AATCCATACATATCCCTTTTGGACCAAGACTCGTTTCAATGAGCTTCAGGGAACCA 1723
DB 839 AATCCTTCTATGTCGCACTTCTTGAAGTACACAGACTCAGAACTGATCTGGGCGCA 898
QY 1724 ATGTGCTCGGCTGACAGTATACGTGGCTTCTTGACACGGCCACTCGAACCGTGCATT 1783
DB 899 ATGTACCCCGTCCACACAGTTTGGCGATGCTCTCTCAACACCATCTCACACCGTGCATC 958
QY 1784 ACTACTGG 1791
DB 959 GTTACTGG 966

RESULT 8
AV792419/c
LOCUS
DEFINITION
AV792419 RAFL7 Arabidopsis thaliana cDNA clone RAFL07-14-P04 3',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
AV792419 433 bp mRNA linear EST 29-MAR-2002
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 433)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Ono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@tc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda PCL-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web

site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source Location/Qualifiers
1..433
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAPL07-14-P04"
/dev_stage="rosette plants"
/lab_host="DH10B"
/clone_lib="RAPL7"
/note="Site 1: BamHI; Site 2: SalI; subjected to cold-treated (1, 2, 5, 10, 24 hr)"

ORIGIN

Query Match 19.8%; Score 432; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 7.2e-92;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1718 ACCAATGTGCTCGCCCTGACAGTATACGTGCTTCTTGACACGCCCACTCGAACCG 1777
433 ACCAATGTGCTCGCCCTGACAGTATACGTGCTTCTTGACACGCCCACTCGAACCG 374
1778 TGCATTACTGAGACAATTTGATGACTCTTCATGCGACCGCTTTGGAGGTCGTG 1837
373 TGCATTACTGAGACAATTTGATGACTCTTCATGCGACCGCTTTGGAGGTCGTG 314
1838 GCTTTGACCTTTGTTCCAGGTTCTCAACTGAGAGAAACCTCTCTGATCTTAGTAAGG 1897
313 GCTTTGACCTTTGTTCCAGGTTCTCAACTGAGAGAAACCTCTCTGATCTTAGTAAGG 254
1898 CTTGAGGTTACGTTGGAAGAAAGCTTTGATTTTGTGTAGAAAGGTTGATCAAAAT 1957
253 CTTGAGGTTACGTTGGAAGAAAGCTTTGATTTTGTGTAGAAAGGTTGATCAAAAT 194
1958 TATGCTTTGTTGTAATATCAATTTGATATATTTGTTGAGACAGAAATCTGTCCTA 2017
193 TATGCTTTGTTGTAATATCAATTTGATATATTTGTTGAGACAGAAATCTGTCCTA 134
2018 ACGTTTGTAGAGACAGAAAGCAAAACATGCGCACTTTGAAGTGTTCATGATGATGTA 2077
133 ACGTTTGTAGAGACAGAAAGCAAAACATGCGCACTTTGAAGTGTTCATGATGATGTA 74
2078 TTATATTCATATTTGTTGTTGTAACAACTACACATTTGTTGTTGTTGTTGTTGTTG 2137
73 TTATATTCATATTTGTTGTTGTAACAACTACACATTTGTTGTTGTTGTTGTTGTTG 14
2138 GTTTTGTCTTCG 2149
13 GTTTTGTCTTCG 2

RESULT 9

AV825792 629 bp mRNA linear EST 01-APR-2002
AV825792 RAPL7 Arabidopsis thaliana cDNA clone RAFL07-14-P04 5',
mRNA sequence.
AV825792
AV825792.1 GI:19867852
EST.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 629)
Seki, M., Narusaka, M., Iehida, J., Kamiya, A., Satou, M., Nakajima, M.,
Ono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki

REFERENCE

CD531888 448 bp mRNA linear EST 31-DEC-2003
12622 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA
3', mRNA sequence.
CD531888
CD531888.1 GI:40451900
EST.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana

TITLE

JOURNAL
COMMENT

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-9060

Email: msekic@riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source Location/Qualifiers
1..629
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAPL07-14-P04"
/dev_stage="rosette plants"
/lab_host="DH10B"
/clone_lib="RAPL7"
/note="Site 1: BamHI; Site 2: SalI; subjected to cold-treated (1, 2, 5, 10, 24 hr)"

ORIGIN

Query Match 19.7%; Score 429.4; DB 1; Length 629;
Best Local Similarity 98.0%; Pred. No. 3.2e-91;
Matches 433; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
1 CCTCTCTGTTTCCTGCTAGACGAAAGAAATCTCAGGTTTGTAGCTTTTCA 60
187 CCTCTCTGTTTCCTGCTAGACGAAAGAAATCTCAGGTTTGTAGCTTTTCA 246
61 AGCTTCCAAAATTTTGAATTTTGTATCTTCTGGGCTCTTTTGAATCAGACTGAAGATAT 120
247 AGCTTCCAAAATTTTGAATTTTGTATCTTCTGGGCTCTTTTGAATCAGACTGAAGATAT 306
121 TTAGATTATCCCAAGAGTTTGTCAAGAAATGTTTCAGTGGACGACGCAAGAAAGTAAAG 180
307 TTAGATTATCCCAAGAGTTTGTCAAGAAATGTTTCAGTGGACGACGCAAGAAAGTAAAG 366
181 AGACTTTTTTTCAGATTTTGTCTGATCCAAATCTGAATAGTTTCTCATGTTCTTGGAT 240
367 AGACTTTTTTTCAGATTTTGTCTGATCCAAATCTGAATAGTTTCTCATGTTCTTGGAT 426
241 CAAATCTGGAAGAGAAAGTTTGTGGATCTAGAAAGATAAACAATGTTGGATTTCTCTA 300
427 CAAATCTGGAAGAGAAAGTTTGTGGATCTAGAAAGATAAACAATGTTGGATTTCTCTA 486
301 GTGCGAAACTGCTTCGTTATCGACATCTGATCAGCTTCTGTGTCGTTGCGTTGAATCTC 360
487 GTGCGAAACTGCTTCGTTATCGACATCTGATCAGCTTCTGTGTCGTTGCGTTGAATCTC 546
361 TTTGTTGCACTTCTTTGCTGTTGTTATTTCTTGTGTCATCTTTTGGAAAGATAGATGG 420
547 TTTGTTGCACTTCTTTGCTGTTGTTATTTGTTGTCATCTTTTGGAAAGATAGATGG 606
421 ATGACGAATCCATCCACCGCT 442
607 GTGAACGAATCCATCCACCGCT 628

RESULT 10

CD531888
LOCUS
DEFINITION
12622 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA
3', mRNA sequence.
CD531888
CD531888.1 GI:40451900
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 448)

| REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT |
|-----------|---------|-------|---------|---------|
| 1 | ... | ... | ... | ... |
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FEATURES

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Location/Qualifiers
1. .448
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/scot_type="Landsberg erecta"
/db_xref="taxon:3702"
/tissue_type="Leaf"
/dev_stage="Yellow Leaf With Gre
/lab_host="E. coli"
/clone_lib="Arabidopsis Leaf Sen
/notes="Organ: Rosette Leaf; Vect
Site 1: EcoRI; Site 2: EcoRI; Se
and #6 (counted from the bottom)
Immediately frozen in liquid N2.
yellow excepted for the leaf bas
greenish.

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ORIGIN

| Query Match | 19.4%; | Score 422.4; | DB 6; | Length 448; |
|-----------------------|---|--------------------|-----------|-------------|
| Best Local Similarity | 99.3%; | Prod. No. 1.4e-89; | | |
| Matches 445; | Conservative 0; | Mismatches 1; | Indels 2; | Gaps 2; |
| 1615 | CGCACGAGAACGCCACACGAGCATGTTATCTGATGACAACACCCCAAAATCCATACAT | 1674 | | |
| 1 | CGCACGAGAACGCCACACGAGCATGTTATCTGATGACAACACCCCAAAATCCATACAT | 60 | | |
| 1675 | ATCCCTTT-GTTGGACCAAGACTCGTTTCATTTGAGCCTTCAGGGNAACACAATGTGCCTCG | 1733 | | |
| 61 | ATCCCTTTGTTGGACCAAGACTCGTTTCATTTGAGCCTTCAGGGNAACACAATGTGCCTCG | 120 | | |
| 1734 | GCCTGACAGTATACGTGGCTCTTTTGACACGGCCACCTCGAAACCGTGCAITTACTACTCGAG | 1793 | | |
| 121 | GCCTGACAGTATACGTGGCTCTTTTGACACGGCCACCTCGAAACCGTGCAITTACTACTCGAG | 180 | | |
| 1794 | ACAATTTGATGACTCCTTCATGGCAACCCGTCCTTTGGAGGTCGTGGCTTTGTACCCCTTGT | 1853 | | |
| 181 | ACAATTTGATGACTCCTTCATGGCAACCCGTCCTTTGGAGGTCGTGGCTTTGTACCCCTTGT | 240 | | |
| 1854 | TCCAGGTTCTCCAACTGAGAGAAACCCCTCCTGATCTTAGTAAGGCTTGAGGTAACGCTGG | 1913 | | |
| 241 | TCCAGGTTCTCCAACTGAGAGAAACCCCTCCTGATCTTAGTAAGGCTTGAGGTAACGCTGG | 300 | | |
| 1914 | AGAAAAGCTTTGA - TTTTTTTTGGTAGAAAAAGGCGATTCAAATATAGCTTTTGTGTAA | 1972 | | |
| 301 | AAGAAAAGCTTTGATTTTTTTTTTGGTAGAAAAAGGCGATTCAAATATAGCTTTTGTGTAA | 360 | | |
| 1973 | ATTATCCATTTGTAAATATCTTTGTGAGGACAGAAATCTGCTCTTAACGTTTTTGAGACGAG | 2032 | | |
| 361 | ATTATCCATTTGTAAATATCTTTGTGAGGACAGAAATCTGCTCTTAACGTTTTTGAGACGAG | 420 | | |
| 2033 | AAAGCAAAACATCGCAACTTTTGAAGTGT | 2060 | | |
| 421 | AAAGCAAAACATCGCAACTTTTGAAGTGT | 448 | | |

RESULT 11

BU004460
LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISATION

REFERENCE
AUTHORS

| TITLE | JOURNAL | COMMENT |
|---|---------------------------------|-----------------------------------|
| 1. The Role of the Teacher in the Classroom | Journal of Educational Research | 1980, Vol. 83, No. 1, pp. 1-10 |
| 2. The Impact of Technology on Education | Journal of Educational Research | 1980, Vol. 83, No. 2, pp. 11-20 |
| 3. The Importance of Parental Involvement | Journal of Educational Research | 1980, Vol. 83, No. 3, pp. 21-30 |
| 4. The Effect of Teacher Expectations on Student Achievement | Journal of Educational Research | 1980, Vol. 83, No. 4, pp. 31-40 |
| 5. The Role of the School in the Community | Journal of Educational Research | 1980, Vol. 83, No. 5, pp. 41-50 |
| 6. The Impact of Socioeconomic Status on Student Achievement | Journal of Educational Research | 1980, Vol. 83, No. 6, pp. 51-60 |
| 7. The Role of the Teacher in the Classroom | Journal of Educational Research | 1980, Vol. 83, No. 7, pp. 61-70 |
| 8. The Impact of Technology on Education | Journal of Educational Research | 1980, Vol. 83, No. 8, pp. 71-80 |
| 9. The Importance of Parental Involvement | Journal of Educational Research | 1980, Vol. 83, No. 9, pp. 81-90 |
| 10. The Effect of Teacher Expectations on Student Achievement | Journal of Educational Research | 1980, Vol. 83, No. 10, pp. 91-100 |

FEATURES
source

```

1. .733
location/Qualifiers
/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="L. serriola"
/db_xref="taxon:4236"
/clone="QGG5E06"
/lab_host="E.coli"
/clone_lib="QG_EFGHJ lettuce serriola"
/notes="Vector: pRCNDSFIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu
TAG TISSUE=flowers environmental stress
TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=CGATGCGG"

```

ORIGIN

| | Query Match | 19.1%; | Score 416.6; | DB 5; | Length 733; |
|----|-----------------------|---|--------------------|-----------|-------------|
| | Best Local Similarity | 75.4%; | Pred. No. 3.7e-88; | | |
| | Matches 518; | Conservative 0; | Mismatches 169; | Indels 0; | Gaps 0; |
| Qy | 323 | CGACATCTGATCAGCGTTCTGTGGTTCGCTTGAATCTCTTTGTGTGACACTCTTTGTGCACTTCTTTGTGCTT | 382 | | |
| Db | 47 | CTACCTCTGNGTACTCTTCCATGTCTCTATGAACCTGTTTGTGTGCTTCTTCTTTGTGCTT | 106 | | |
| Qy | 383 | GTATGTGTTCTTGCTCATCTTTTGGAGAGANAATAGATGGATGGAACGAAATCCATCACCGCCT | 442 | | |
| Db | 107 | GTATCGTAAATCGGTCTATCTTTTGGAAAGAGAATCGATGGATGAACGAAATCTTATCACTGCC | 166 | | |
| Qy | 443 | TGTTTGATTTGGCTTAGGCACCTGGTGTTCACATTTTGTGTGATTAGTAAAGGAAAAAGCTCGC | 502 | | |
| Db | 167 | TTGTCTATTGGTATTGCACCTGGNGTTGTATTTTGTTAAGCACTGGGAGAACAAATTCAC | 226 | | |
| Qy | 503 | ATCTCTCGTCTTTAGTGAAGATCTTTTCTTCATATATCTTTTGCCACCCCATTTATATCA | 562 | | |
| Db | 227 | ATCTTCTAGTCTTCAGTGAAGATCTTTTCTTCATTTATCTTCTTCAACCTTATCATCTTCA | 286 | | |

563 ATGCAGGTTTCAAGTAAAGAGAGAGTTTTCGCCAATTTTCGTCAGTATTATGCTTT 622
 |||||
 287 ATGCTGGGTTTCAGGTTAAGAGAGAAACAATTTTTCGCAATTTTCATGACCAATTTGCTAT 346
 |||||
 623 TTGTGCTGTTGGGACATATTATTTCTTGCGCAATCATATCTCTAGAGGTGAACACAGTTCT 682
 |||||
 347 TTGTGCTGTTGGGACATGATATCTTTTCCACCATCATATCATTTGGTGCTATAAATTT 406
 |||||
 683 TTAAGAGTTGGACATTTGGACCTTTGACTTGGGTGATTTATCTGTTGGTGCCATAT 742
 |||||
 407 TCCAAGAGATGGATTTGGTACCCCTTGAGCTTGGAGACTTTCTTGCAATTTGGTGAATAT 466
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 743 TTGCTGCAACAGAGATTCAGTATGTACACTGCAGGTTCTGAATCAAGACGAGACACCTTTGC 802
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 467 TTTTCAAGCCAGATTCGTTTGCATTTTGCAGGTGTTGAATCAGATCAGACACCTTTAT 526
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 803 TTTACAGTCTTGATTCGAGAGAGGTTTGTGAATGATCAACGTCAGTTGTTGCTTTCA 862
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 527 TATATAGTTTGGTGTGGTGAAGGTGTGGTGAATGATGCCACATCAGTTGTCTATCTTCA 586
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 863 ACGGATTCAGAGCTTTGATCTCACTCACTCAACACGAGCTGCTTTTTCATCTTCTTG 922
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 587 ATGCAGTTCAAACTTTGATCTCTCTCAATCAACAACCTGCTGTTGCAATTTTCAACTGATTG 646
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 923 GAAACTTCTTGATTTCTTCTTAAGTACCTTGTGCTTGGTGTGCAACCGGCTCGATTA 982
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 647 GAAATTTCTTTATTTATTCATCACAAGCACACTTCTAGAGCTGGAGCTGGGCTACTAA 706
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 983 GTGGGATGTTATCAAGAACTATACT 1009
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 707 GTGCTTATATATAAAGAGCTATATT 733
 |||||

RESULT 12 LOCUS

DEFINITION GR_Eal7A01.r GR_Ea Gossypium raimondii cDNA clone GR_Eal7A01.3', mRNA sequence.

ACCESSION CO094724.1 GI:48793410

VERSION EST.

KEYWORDS Gossypium raimondii

SOURCE Gossypium raimondii

ORGANISM Gossypium raimondii

REFERENCE 1 (bases 1 to 827)

AUTHORS Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C., Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and Wing, R. A.

TITLE Global assembly of Cotton ESTs

JOURNAL Unpublished (2004)

COMMENT Contact: Rod A. Wing

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ, 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: http://genome.arizona.edu

Plate: 17 row: A column: 01.

Location/Qualifiers

1. 827

/organism="Gossypium raimondii"

/mol_type="mRNA"

/db_xref="taxon:29730"

/clone="GR_Eal7A01"

/tissue_type="whole seedlings"

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/lab_host="DH10B"

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/notes="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2: EcoRV; Library made by Invitrogen with RNA supplied by

FEATURES source

ORIGIN

Query Match 19.1%; Score 416.2; DB 7; Length 827;
 Best local similarity 70.5%; Pred. No. 4.7e-88;
 Matches 556; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

QY 973 GGTCATGAAGTCGCTATGTTATCAAGAAGCTATATCTTTGGAGGACCTCAACTGACCGA 1032
 DB 37 GGTTGGTTAGTGTCTTACATCATCAAAAAGTTGTACTTTTGGAGGACCTCAACAGATCGT 96
 QY 1033 GAGTTGCCCTTATGATGCTTATGGCGTATCTTTCTTATATGCTTCTGAGCTTTTCGAC 1092
 DB 97 GAATTTGCTCTTATGATGCTTATGGCAATACCTTTGTAATATCATGCTGAAGCTTTCTAT 156
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 DB 277 GCTGAGACTTTTCTTTCTTTTATGTCGGATGGATGCTTTGGACATGAGAGTGGAGA 336
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RESULT 13

BE420587

LOCUS

DEFINITION

BE420587

ACCESSION

VERSION

BE420587.1

KEYWORDS

BE420587 1212 bp mRNA linear EST 24-JUL-2000
 HWM000.D12 ITC HWM Barley Leaf Library Hordeum vulgare subsp.
 vulgaris cDNA clone HWM000.D12, mRNA sequence.
 BE420587
 BE420587.1 GI:9418430
 EST.

Wendle lab. Directional cloned into NotI-EV. Colonies
 plated/picked by AGI. More glycerol clones held in -80."

SOURCE
ORGANISM
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE
AUTHORS
1 (bases 1 to 1212)
Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.
TITLE
International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
JOURNAL
COMMENT
Unpublished (2000)
Contact: Herrmann RG
Botanisches Institut der LMU
Menzinger Str. 67, D-80638 Munchen GERMANY
Fax: 49 30 171683
Email: hermann@botanik.biologie.uni-muenchen.de
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
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DB 121 CCTTCAGTATATATCACTTGTGTCATGGGCTAGTATCAAGCTGAACATAGGCGCC 180
QY 707 TTGACTTGGGTGATATCTTGTCTATTGTTGCCATATTGCTGCAACAGATTTCAGTATGTA 766
DB 181 TTGAGCTTGGAGACTACCTCGCACTTGGGCAATATCTCGCAACGGACTCTCTTCGCA 240
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QY 887 CTCACCTAAACCAACGAAGCTGCTTTTCACTCTCTTGGAACTTCTTGTATTGTTTCTCC 946
DB 361 GAAATTCAGTAGCCTCAAAATCTTACAAATTCATTCGAAATTTCTCTATCTATTGCGC 420
QY 947 TAAGTACCTTGTGTTGCTGCAACCGGCTGTGATTAAGTGGGTATGTTATCAAGAAGCTAT 1006
DB 421 CCAGTACCTTTCTTGGAGTATCTAGTGGACTTCTCAGTGTGTTATGTCATCAAGAACTGT 480
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DB 481 ACTTTGGAGGCACTCACTGATCGTGAAGTTGCTATTATGATGCTCGGCTATTATTAT 540

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RESULT 14
LOCUS
DEFINITION
CO085721.f GR_Ea Gossypium raimondii cDNA clone GR_Ea03A21 5', mRNA sequence.
VERSION
CO085721.1 GI:48776355
KEYWORDS
Gossypium raimondii
SOURCE
Gossypium raimondii
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eustosids II; Malvales; Malvaceae; Malvaceae; Gossypium. 1 (bases 1 to 827)
REFERENCE
AUTHORS
Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C., Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and Wing, R.A.
TITLE
Global assembly of Cotton ESTs
JOURNAL
COMMENT
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
Plate: 03 row: A column: 21.
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ORIGIN
Query Match 19.1%; Score 415; DB 7; Length 827;


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